

us-09-077-817-12.rag

Sat Sep 1 19:37:55 2001

GenCore version 4.5
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OM protein - protein search, using sw model
September 1, 2001, 19:16:53 ; search time 21.2 seconds
(without alignments)
Run on: 1080.937 Million cell updates/sec

Title: US-09-077-817-12

Perfect score: 2087
Sequence: 1 MAFVCLAIAGLTVFLISTTF.....TGLLRKPNTPKRVCVTL 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2059	98.7	380	AAW24972	Human interleukin-13
2	2059	98.7	380	AAW35295	Human IL-13 bindin
3	2059	98.7	380	AAW35613	Human Zcytor2 cyto
4	2059	98.7	380	AAW41520	Human HR-1 recepto
5	2059	98.7	380	AAW41502	Human cytokine/pep
6	2059	98.7	380	AAW33603	Human IL-13 binding
7	2059	98.7	380	AAW33603	Human IL-13 recept
8	2059	98.7	380	AAW33603	Human Zcytor2 cyto
9	2059	98.7	380	AAW33603	Human IL-13 recept
10	2059	98.7	380	AAW33603	Human Zcytor2 cyto
11	1853	88.8	372	AAW36616	Celebus macaque zc

Mature interleukin
Construct containi
Murine IL-13 bindi
IL-13 binding chai
Murine interleukin
Mouse IL-13 recept
Interleukin-13 bin
Sequence of human
Sequence of secret
Human interleukin-
Human IL-5 recepto
Sequence of human
Protein used in pr
Human interleukin-
Human interleukin-
Human interleukin-
Mouse interleukin-
IL5-R-GBP 130 fusi
Soluble human IL-5
shIL-5R-alpha. Sy
Human interleukin-
IL-13/IL-4 dual tr
Sequence of interl
Sequence of interl
Sequence of interl
Sequence of interl
Sequence of interl
IL-2 receptor gamm
IL-2 receptor gamm
Murine IL-2R gamma
Human cytokine rec

12	1753	84.0	315	19	AAW56261
13	1753	84.0	359	19	AAW56260
14	1194.5	57.2	383	18	AAW35294
15	1194.5	57.2	383	21	AAW35295
16	1194.5	57.2	383	22	AAW72135
17	1194.5	57.2	383	22	AAW29747
18	456	21.8	157	19	AAW56252
19	310.5	14.9	396	13	AAW22216
20	310.5	14.9	396	13	AAW22220
21	310.5	14.9	420	13	AAW22219
22	310.5	14.9	420	13	AAW22218
23	309.5	14.6	420	13	AAW22215
24	304.5	14.6	420	13	AAW22215
25	297	14.2	313	18	AAW21856
26	294.5	14.1	427	18	AAW24973
27	294.5	14.1	427	22	AAW19807
28	293.5	14.1	426	18	AAW09822
29	292.5	14.0	426	18	AAW09821
30	292.5	14.0	1026	16	AAW70121
31	292	14.0	335	13	AAW25063
32	285.5	13.7	793	21	AAW33699
33	284	13.6	784	21	AAW33699
34	284	13.6	784	21	AAW33699
35	242	11.6	398	13	AAW22212
36	241	11.5	415	13	AAW22217
37	241	11.5	415	13	AAW22214
38	229	11.0	332	13	AAW22213
39	229	11.0	332	13	AAW22218
40	229	11.0	332	13	AAW22218
41	229	11.0	367	15	AAW47148
42	219	10.5	347	15	AAW47149
43	209.5	10.0	369	15	AAW50994
44	209	10.0	482	19	AAW31646

ALIGNMENTS

RESULT	1
AAW24972	AAW24972 standard; protein; 380 AA.
ID	AAW24972
XX	AAW24972;
AC	22-JUN-1998 (first entry)
DT	Human interleukin-13 beta receptor.
DE	Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
DE	Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
KW	Homo sapiens.
OS	WO9720926-A1.
PN	12-JUN-1997.
PD	07-NOV-1996; 96WO-FR01756.
XX	06-DEC-1995; 95FR-0014424.
PF	(SNFI) SANOFI SA.
PR	Caput D, Ferrara P, Laurent P, Vita N;
XX	WPI: 1997-319773/29.
XX	N-PSDB: AAW5826, AAW86464.
DR	New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allergy, etc
PT	Claim 1; Figure 2a; 83pp; French.
PT	
XX	
PS	

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R
 CC and alpha which can be used as IL-13 antagonists specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface
 CC are used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).
 XX Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 18; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIGCLYTLISTTFCCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
 Db 1 mafvclaigcltflisttfgctssdteikvnpqdfeidvdpgylylqwqpplsl 60
 QY 61 HFKECTVEYELKYNIGSEWTKITKNLHYKDGFLNKGIEAKHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwtiiknlhkydgdflnkgieakhtllpwqctngse 120
 QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWOYLCSKPKGIGVLLDPNNLFYWEGLDH 180
 Db 121 sswaettywispqipetkvdmdcvynnwylcswkpgigvllldpnnlfiwyegldh 180
 QY 181 ALOCVDYIKADGNTGCRPPYLEASDYKDFYICVNGSSENKPIRSSYFFQONTVKPLP 240
 Db 181 alqcvdylkadgntgcrpfyleasykdfyicvngssenkprrsyffqontvklp 240
 QY 241 PVLNFTRESCEIKLWSIPLGPIPARCFDYEIEFREDDTLTVATVENETYTLKTNE 300
 Db 241 pylvnftresceiklwsiplgpiparcfdyeiiefreddtlvtatvenetytlkt 300
 QY 301 TRQLCFVRSKVNITYCSDGIRSEWSKOCWEGEDLSKTLRLFWLPFGFILILVFTG 360
 Db 301 trqlcfvrskvnitycsdgiwsewskgcwgedlskttlrlfwlpfgfllilvftg 360
 QY 361 LLLRKPNTPKMW 373
 Db 361 llrkpntpkmi 373

RESULT 2

AAW35295
 ID AAW35295 standard; Protein; 380 AA.
 AC AAW35295;
 XX
 DT 27-MAR-1998 (first entry)
 XX Human IL-13 binding chain of the IL-13 receptor.
 DE Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.
 XX

OS Homo sapiens.
 XX Key
 FH Peptide
 FT Location/Qualifiers
 FT 1..25
 FT /label= signal_sequence
 FT 26..380
 FT /note= "putative"
 FT Protein
 FT 26..341
 FT /label= mature_protein
 FT Domain
 FT 342..362
 FT /label= extracellular_domain
 FT Domain
 FT 363..380
 FT /label= transmembrane_domain
 FT Domain
 FT /label= intracellular_domain
 XX WO9731946-A1.
 XX 04-SEP-1997.
 XX 28-FEB-1997; 97WO-US03124.
 XX 01-MAR-1996; 96US-0609572.
 XX (GENY) GENETICS INST INC.
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;
 XX WPI; 1997-448632/41.
 XX N-PSDB; AAT95214.
 XX New nucleic acid encoding interleukin-13 receptor binding chain and
 XX transformed cells - proteins antibodies and inhibitors, for
 XX treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 XX and in diagnosis
 XX Claim 11; Pages 34-35; 49pp; English.
 XX The present sequence represents the human interleukin-13 (IL-13) binding
 XX chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 XX mediator of the known biological activities of IL-13. Recombinant
 XX IL-13bc proteins, and antibodies raised against them, are used to
 XX inhibit the binding of IL-13 to its receptor. They are particularly used
 XX to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 XX disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 XX They are also used to treat immune deficiency (particularly in
 XX haematopoietic progenitor cells), cancer etc., and to increase macrophage
 XX activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 XX in vivo, to a cell expressing at least one chain of the IL-13 receptor,
 XX other than IL-13bc, IL-13bc can also be used in diagnosis to detect
 XX expression of IL-13, its receptor or binding chain, and to raise specific
 XX antibodies which may be useful for treating some tumours.
 SQ Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 18; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIGCLYTLISTTFCCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
 Db 1 mafvclaigcltflisttfgctssdteikvnpqdfeidvdpgylylqwqpplsl 60
 QY 61 HFKECTVEYELKYNIGSEWTKITKNLHYKDGFLNKGIEAKHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwtiiknlhkydgdflnkgieakhtllpwqctngse 120
 QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWOYLCSKPKGIGVLLDPNNLFYWEGLDH 180
 Db 121 sswaettywispqipetkvdmdcvynnwylcswkpgigvllldpnnlfiwyegldh 180

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QY 181 ALQCVDIKADGQNGICRFPYLEASDKYKDFYICVNGSSENKPIRSSYFTFOLQNIIVKPLP 240
Db 181 alqcvdyikadgqngicrfyleasdykdfyicvngssenkpirssyftfqlqnlvixp 240
QY 241 PVIYTFRESSCEIKLWSIPLGPIPARCFDYETEIREDDDTLTATVENETYTLKTNE 300
Db 241 pviytfressceiklwsiplgpiparcfdyeteiredddtltatvenetytlktne 300
QY 301 TRQLCFVVRKSVNIYCSDDGIWSWSKQCEGSDLSKTLRLFWLPFGFILLIVIFVTG 360
Db 301 trqlcfvvrsvnlycsddgiwswskqcegedlskktllrflwlpfgfllilvifvtg 360
QY 361 LLLRKPNTYPKMW 373
Db 361 llrrkpnntypkmi 373

RESULT 3
AAW36613
ID AAW36613 standard; Protein; 380 AA.
XX AC AAW36613;
XX DT 30-MAR-1998 (first entry)
XX DE Human Zcytor2 cytokine receptor protein.
XX KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
XX KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 340..363
XX FT Domain /label= transmembrane_domain
XX FT Domain 364..380
XX FT Domain /label= intracellular_domain
XX FT Domain 25..339
XX FT Domain /label= ligand_binding_domain
XX PN W09733913-A1.
XX PD 18-SEP-1997.
XX PF 12-MAR-1997; 97WO-US04043.
XX PR 13-MAR-1996; 96US-0013345.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
XX PI O'Hara PU;
XX DR WPI; 1997-470820/43.
XX DR N-PSDB; AAT96782.
XX PT New nucleic acid encoding testis-specific cytokine receptor - useful
XX PT for identification of ligands or antagonists, potentially for use as
XX PT male contraceptives or for infertility treatment
XX PS Claim 2; Page 47-48; 79pp; English.
XX CC This sequence represents a novel ligand-binding receptor, Zcytor2,
XX CC which shares homology with cytokine receptors and was isolated from human
XX CC placental polyA+ RNA. The resulting polypeptide is a receptor for
XX CC cytokines (particularly interleukin-13) and is expressed on the surface
XX CC of testicular cells, probably being involved in spermatogenesis. It can
XX CC be used to detect ligands that promote proliferation and/or
XX CC differentiation of such cells in cultures and may also be used to treat
XX CC infertility. Antagonists of this receptor may be used to characterise
XX CC ligand-receptor interactions and as male-specific contraceptives. By
XX CC blocking the action of IL-13, receptor antagonists and ligand-binding
XX CC this receptor can also be used to modulate immune function, e.g. in
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CC allergy and asthma, as a diagnostic to determine circulating levels of
CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.
XX SQ Sequence 380 AA;
Query Match 98.7%; Score 2059; DB 18; Length 380;
Best Local Similarity 99.7%; Pred. No. 3.5e-193;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTFELISTTFCSTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPISLD 60
Db 1 mafvclaigcltyflisttfcstssdteikvnpqdfelvdpgylglylylqwppisld 60
QY 61 HFKECTVEYELKYRNIGSEWTKTIITKNLHYKDGFDLKNKGIEAKIHTLLPQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwtiitknlhykdgfdlnkgleakihltllpwctngsevg 120
QY 121 SSWAETTYWISPGQIPETKVQDMDCVYNNWOYLCSNKPQIGVLLDTNYNLFYWEGLDH 180
Db 121 sswaettywispgqipetkvqdmcdvynnwoyllcsnkpqigvlldtynnlfywegldh 180
QY 181 ALQCVDIKADGQNGICRFPYLEASDKYKDFYICVNGSSENKPIRSSYFTFOLQNIIVKPLP 240
Db 181 alqcvdyikadgqngicrfyleasdykdfyicvngssenkpirssyftfqlqnlvixp 240
QY 241 PVIYTFRESSCEIKLWSIPLGPIPARCFDYETEIREDDDTLTATVENETYTLKTNE 300
Db 241 pviytfressceiklwsiplgpiparcfdyeteiredddtltatvenetytlktne 300
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Db 301 trqlcfvvrsvnlycsddgiwswskqcegedlskktllrflwlpfgfllilvifvtg 360
QY 361 LLLRKPNTYPKMW 373
Db 361 llrrkpnntypkmi 373

RESULT 4
AAW41520
ID AAW41520 standard; Protein; 380 AA.
XX AC AAW41520;
XX DT 22-JUN-1998 (first entry)
XX DE Human HR-1 receptor.
XX KW HR-1 receptor; human; cytokine; infection; asthma; allergy;
XX KW haematopoietic disorder; tumour; therapy; diagnosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Protein /label= Sig_peptide
XX FT Protein 22..380
XX FT Protein /label= Mat_protein
XX PN W09747741-A1.
XX PD 18-DEC-1997.
XX PF 12-JUN-1996; 96WO-US10262.
XX PR 12-JUN-1996; 96WO-US10262.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
```

XX PI Appelbaum ER, Hu J;
 XX KW WPI: 1998-052308/05.
 XX DR N-PSDB; AAV04131.
 XX
 XX Nucleic acid sequence encoding human cytokine peptide hormone
 PT receptor - useful to treat, prevent or diagnose, e.g. lowered
 PT resistance to infection, asthma, allergy or haematopoietic disease
 XX
 XX Claim 13; Page 62-64; 76pp; English.
 XX
 XX This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated the HR-1 receptor, that shows 27% identity
 CC and 52% similarity to the interleukin-5 receptor. Its amino acid
 CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
 CC human testis library. Recombinant HR-1 receptor can be expressed
 CC in claimed host cells, and used in a claimed method for identifying
 CC compounds which bind to, and activate or inhibit, it. HR-1
 CC receptor activators and agonists can be used to treat, prevent or
 CC diagnose predisposition to lowered resistance to infection, asthma,
 CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
 CC aplastic anaemia, neutropaenia or cytotoxic treatments for cancer.
 CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
 CC be used to treat conditions associated with HR-1 receptor
 CC overexpression. The antibodies can also be used to determine HR-1
 CC receptor levels, since overexpression may be diagnostic of tumours.
 XX
 XX Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 19; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPQPQDFEIVDPGVLGYLYLQWQPPPLSLD 60
 Db 1 mafvclaigcltytlstftgctssdteikvnpqpqdfeidvpgylglylylqwppplsl 60
 Qy 61 HFKECTVEYELKYRNIGSETWKTITKNLHYKDGFDLNKGEAKIHLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitknlhkdgfdlnkgeakihllpwqctngsevg 120
 Qy 121 SSWAETTYWISPGQIPETKVDMDCVYNNQYLLCSWKPQIGVLLDTNLYNFWYEGLDH 180
 Db 121 sswaettywispqgipetkvdmdcvynnwqyllcswkpgigvlldtntnlyfwyegldh 180
 Qy 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
 Db 181 alqcvdylkadqngicrfpyleasdykdfyicvngssenkprrsyftfqlqnvkplp 240
 Qy 241 PVLTLFTRESSECEIKLWSIPGLPAPRCFDYEIEIRDDTTLTAVENETYTKTNE 300
 Db 241 pylvltftresseceiklwsipglpaprctdyeieirddtltlatvenetytktne 300
 Qy 301 TRQLCFVVRKVNIVYCSDDGIWSEWSKQCEGEDLSKKTLLRFLWLPFGFTLILVIFVTG 360
 Db 301 trqlcfvvrskvnivcsddgiwsewsdkqcegedlskktllrflwlpfgftlilvifvtg 360
 Qy 361 LLLRRKPNTPYKMW 373
 Db 361 llrrkpnptypkmi 373

RESULT 5
 AA41502
 ID AA41502 standard; Protein; 380 AA.

XX
 AC AA41502;
 XX
 DT 08-JUN-1998 (first entry)
 DX
 DE Human cytokine/peptide receptor, HR-1 receptor.

XX
 KW HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
 KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
 KW neutropaenia; therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= Sig_peptide
 FT Protein 22..380
 FT /label= Mat_protein
 FT /note= "Claim 14"
 XX
 XX EP812913-A2.
 XX
 XX 17-DEC-1997.
 XX
 XX 04-JUN-1997; 97EP-0303815.
 XX
 XX 12-JUN-1996; 96US-0017843.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Appelbaum ER, Hu J;
 XX
 XX WPI: 1998-034974/04.
 XX N-PSDB; AAV04075.
 XX
 XX Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
 PT increase resistance to infections in individuals with trauma and/or
 PT burns
 XX
 XX Claim 13; Page 27-28; 34pp; English.

XX This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated HR-1 receptor. The amino acid sequence
 CC was deduced from a cDNA clone (see AAV04075) isolated from a human
 CC testis cDNA library. It shows 27% amino acid identity and 52%
 CC similarity with the human interleukin-5 receptor. Also claimed are
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an
 CC antagonist to the polypeptide, antibody against the polypeptide, an
 CC antagonist that inhibits the activity of the polypeptide, a process
 CC for diagnosing a disease, or a susceptibility to disease, related
 CC to expression of HR-1 receptor, and a method for identifying
 CC compounds that activate or inhibit the HR-1 receptor. HR-1
 CC receptor protein and polynucleotides can be used for research,
 CC biological, diagnosis and (gene) therapy applications, e.g. to
 CC increase resistance to infections in individuals with trauma and/or
 CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
 CC predisposition to asthma, allergic disorders or disorders of
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
 CC cyclic neutropaenia or as a consequence of cytotoxic therapy of
 CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.
 XX
 XX Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 19; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPQPQDFEIVDPGVLGYLYLQWQPPPLSLD 60
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Db 181 alqcvdyikadgngicrfyleasdykdfyicvngssenkiprissyftfqlqnvkplp 240
Qy 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIREDDTLTVATVENETYTLKTTNE 300
Db 241 pvyltftressceiklwsiplgpiparcfdyeireddttlvtatvenetytlktne 300
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Db 301 trqlcfvvrskvniycsddgiwsesdkqwegedlskktllrflwlpfgfillivifvtg 360
Qy 361 LLRKPNTPYKMW 373
Db 361 llrkpnptypkmi 373

RESULT 6
AAW33603
ID AAW33603 standard; Protein; 380 AA.
XX AC AAW33603;
XX 08-JUN-1998 (first entry)
XX Homo sapiens HR-1 receptor.
DE Cytokine; hormone receptor; AIDS; acquired immune deficiency;
KW syndrome; aplastic anaemia; neutropaenia; cancer treatment;
KW immune resistance; diagnosis; tumours; HR-1 receptor;
KW asthma; allergic; haematopoietic; disorder.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
XX WO9747742-A1.
XX 18-DEC-1997.
XX 09-JUL-1996; 96WO-US11459.
XX 12-JUN-1996; 96WO-US10262.
XX 12-JUN-1996; 96US-0017843.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX Appelbaum ER, Hu J;
XX WPI; 1998-052309/05.
DR N-PSDB; AAV02295.
XX DNA encoding human cytokine-peptide hormone receptor - useful for
PT treating preventing or diagnosing, e.g. lowered resistance to
PT infection, asthma, allergy, or haematopoietic disease
XX Claim 15; Fig 1; 75pp; English.
XX The sequence is that of the human cytokine/peptide hormone receptor
CC (HR-1 receptor). This, or it's activators or agonists, can be used to
CC treat, prevent or diagnose predisposition to lowered resistance to
CC infection, asthma, allergic or haematopoietic disorders, e.g. where
CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
CC neutropaenia or cytotoxic treatments for cancer. Antagonists of the
CC receptor, e.g. antibodies or fragments of it may be used to treat
CC conditions associated with overexpression of the HR-1 receptor, e.g.
CC those listed above. Antibodies may also be used to assay levels of HR-1
CC receptor, overexpression of which may be diagnostic of tumours, by usual
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CC immunocassays; to isolate and identify HR-1 receptor-expressing cells; or
CC for affinity purification of the HR-1 receptor.
SQ Sequence 380 AA;
Query Match 98.7%; Score 2059; DB 19; Length 380;
Best Local Similarity 99.7%; Pred. No. 3.5e-193;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFVCLAIAGCLYTLISTFTGCTSSSTEIKVNPQDPEIVDPGVLGYLYLQWOPPLSLD 60
Db 1 mafvclaiagclytlistftgctsssteikvnpqdfeiwdpgylylqwapplslid 60
Qy 61 HFKECTVEYELKYRNIGSETWKTITITKLNHYKDGFDLNKIEAKIHTLLPQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwktititknlhykdgfdlnkgleakihltllpqctngsevq 120
Qy 121 SSWAETTYWISPOGIPETKVQMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH 180
Db 121 sswaettywispgipetkvqmdcvynwqyllcswkpgigvlltdtnynlfywyegldh 180
Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadgngicrfyleasdykdfyicvngssenkiprissyftfqlqnvkplp 240
Qy 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIREDDTLTVATVENETYTLKTTNE 300
Db 241 pvyltftressceiklwsiplgpiparcfdyeireddttlvtatvenetytlktne 300
Qy 301 TRQLCFVVRSKVNIYCSDDGIWSWSKQWEGEDLSKKTLLRFWLPFGFILLIVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsesdkqwegedlskktllrflwlpfgfillivifvtg 360
Qy 361 LLRKPNTPYKMW 373
Db 361 llrkpnptypkmi 373

RESULT 7
AAW95296
ID AAW95296 standard; Protein; 380 AA.
XX AC AAW95296;
XX 12-SEP-2000 (first entry)
XX IL-13 binding chain of human IL-13 receptor.
XX Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; antiallergic;
KW antiinflammatory; antiasthmatic; vaccine.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..25
FT /note= "signal peptide"
FT Protein 26..380
FT /note= "mature protein"
FT Domain 26..341
FT /note= "extracellular domain; a polypeptide
FT comprising amino acids 22-334 is
FT specifically claimed in Claim 11(e)"
FT Domain 342..362
FT /note= "transmembrane domain"
FT Domain 363..380
FT /note= "intracellular domain; a polypeptide
FT comprising amino acids 257-383 is
FT specifically claimed in Claim 11(f)"
XX
```

PN W0200036103-A1.
 XX 22-JUN-2000.
 XX 13-DEC-1999; 99WO-US29493.
 XX 14-DEC-1998; 98US-0211335.
 XX (GEM) GENETICS INST INC.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 PI Wills-Karp M;
 XX WPI: 2000-431587/37.
 XX N-PSDB; AAA27912.
 DR New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
 XX an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
 XX asthma, Grave's disease and inflammatory conditions of the lung -
 XX Claim 11(d); Page 53-54; 60pp; English.
 XX The present sequence is that of the interleukin-13 binding chain
 CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated
 CC human testis cDNA clone (see AAA27912). IL-13bc is a member of
 CC the haematopoietin receptor family that acts as a mediator of
 CC IL-13. The invention provides methods for the recombinant
 CC production of IL-13bc polypeptides, including claimed full-length
 CC IL-13bc, its extracellular domain, and its intracellular domain.
 CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
 CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
 CC of IL-13 and its receptor) can be used to treat conditions in
 CC which IL-13 is implicated, particularly IgE-mediated conditions and
 CC diseases including atopy, allergy, asthma, immune complex diseases
 CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
 CC thyroiditis and Grave's disease), lung inflammation,
 CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
 CC activation, IL-13bc proteins can also be used to enhance macrophage
 CC activation, e.g. in vaccination, treatment of mycobacterial or
 CC intracellular organisms or parasite infections. IL-13bc proteins
 CC may also be used to potentiate the effects of IL-13 in vitro and
 CC in vivo, as diagnostic agents, and to screen for agents capable of
 CC binding to IL-13bc or IL-13 receptor, or which interfere with the
 CC binding of IL-13 to its receptor.
 XX SQ Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 21; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

Qy 1 MAFVCLALGCLYTLSTTCTGCTSSDTEIKVNPQDFEIVDPGVLGYLYQWQPPPLSLD 60
 Db 1 mafvclalgclytlsttctgctssdteikvnpqdfeidvdpvglylylqwppplsl 60
 Qy 61 HFKECTVEYELKYNIGSETWKTITKLNHYKDGFDLKNKGTEAKIHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitklnhykdgfdlnkngteakihtllpwqctngsevg 120
 Qy 121 SSWAETTYWISPGQIPETKVDMDVCYVNNQYLLCSMKPGIGVLLDTNLYNLFYWYEGLDH 180
 Db 121 sswaettywispgqipetkvdmdcvynnyqyllcskpgigvlltdntnlynyfwyegldh 180
 Qy 181 ALQCVDIKADQNGICRFPYLEASDKDFYICVNGSENKPIRSSFTFQQLQNVKPLP 240
 Db 181 alqcvdyikadgngicrfpyleasdkdfyicvngssenkiprissyftfqlqnvkplp 240
 Qy 241 PVIYLTFTRESSCEIKLWSIFLGPPIPARCFDYETEIRDDFTLTATVENETYTLKTTNE 300
 Db 241 pviyftressceiklwsiflpgpiparcfdyeteirddftltatvenetytlktne 300

Qy 301 TROLCFVVRSKVNIYCSDDGIWSEWSDKQWEGEDLSKKTLLRFLWLPFGFLILVIFVTG 360
 Db 301 trqlcfvvrskvniycsddgiwsewskqwegedlskktllrflwlpfgflilvifvtg 360
 Qy 361 LLRLKPNTPYKMW 373
 Db 361 llrlkpntpykmi 373
 RESULT 8
 AAY72136
 ID AAY72136 standard; Protein; 380 AA.
 XX AC AAY72136;
 XX DT 24-APR-2001 (first entry)
 XX Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
 DE Human; IL-13; interleukin-13 binding chain of IL-13 receptor; IL13bc;
 XX therapy; tissue fibrosis; Schistosoma infection; surgical incision;
 KW cytostatic; wound; IL-13 related condition; allergic condition;
 KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;
 KW macrophage activation.
 XX Homo sapiens.
 OS
 PH Key Location/Qualifiers
 FT Peptide 1..25 /label= Signal_peptide
 FT Region 1..81 /note= "this region is identical to the translated
 FT sequence of an expressed sequence tag (EST) identified
 FT as Y99f10.r1 human cDNA clone 41648 5"
 FT Protein 26..380 /label= Mature_human_interleukin (IL)-13_binding_chain_
 FT of_IL-13_receptor
 FT Domain 26..341 /note= "Extracellular domain; this region is specifically
 FT claimed in claims 1e, 6e, 15e and 23e"
 FT Domain 342..362 /note= "Transmembrane domain"
 FT Domain 363..380 /note= "Intracellular domain; this region is specifically
 FT claimed in claims 1f, 6f, 15f and 23f"
 XX W0200078336-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-US17103.
 XX 21-JUN-1999; 99US-0334512.
 XX (GEM) GENETICS INST INC.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 XX Wills-Karp M;
 XX WPI: 2001-080753/09.
 XX N-PSDB; AAD02335.
 XX Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
 PT in a mammalian subject, involves administering a pharmaceutical
 PT composition comprising IL-13 antagonist -
 XX Claim 1a; Page 69-70; 72pp; English.
 XX The invention relates to a method of treating, or inhibiting
 CC the formation of tissue fibrosis in mammals, which involves
 CC administering a pharmaceutical composition comprising interleukin
 CC (IL)-13 antagonist. The protein of the invention is useful for

CC treating tissue fibrosis resulting from infection with Schistosoma
 CC or from healing of a wound which is a surgical incision, or
 CC inhibiting formation of tissue fibrosis which affects tissues such
 CC as liver, skin epidermis and endodermis, muscle, tendon, cartilage,
 CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
 CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,
 CC biliary tract and gut. It is also used in the treatment or modulation
 CC of various IL-13 related conditions such as allergic conditions,
 CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.
 CC The present sequence is human interleukin (IL)-13
 CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used
 CC to potentiate the effects of IL-13. This protein is also used to
 CC enhance macrophage activation and hence can be used in vaccination
 CC or treatment of mycobacterial or parasitic infections.

XX Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 22; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLISTTFCCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPPLSLD 60
 Db 1 mafvclaigcllytlsttfgctssdssteikvnpqdfvdpvglylylqwppplsl 60

QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNKGIKIAKHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktititknlyhkgdgdlnkgleakhtllpwqctngse 120

QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
 Db 121 sswaettywispgipetkvdmdcvynwqyllcswkpgigvlltdnynlfywegldh 180

QY 181 ALQCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNVKPLP 240
 Db 181 alqcvdyikadgqngicrfyleasdykdfyicvngsenkpirssyftfqlqnvkplp 240

QY 241 PVIYFTFRESSCEIKLWSIPGLPIPARCFDYIEIRDEDTTLVATVENETYTLKTTNE 300
 Db 241 pviyftfressceiklwsipglpigarcfdyieirddtllvatvenetytlktne 300

QY 301 TRQJCFVVRKVNICYSDDGIWSEWSKQWEGEDLSKTLRLFWLPGFTLILVIFVTG 360
 Db 301 trqlcfvvrskvniycsddgiwsewsdkqwegedlsktlrlfwlpgftlilvifvtg 360

QY 361 LLRKPNTPYKMW 373
 Db 361 llrkpntypkmi 373

RESULT 9
 AAB29748

ID AAB29748 standard; Protein: 380 AA.

XX AC AAB29748;

XX DT 23-FEB-2001 (first entry)

XX DE Human IL-13 receptor IL-13 binding chain (IL-13bc).

XX KW Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
 KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnerary;
 KW wound healing; schistosoma infection; liver; skin; muscle;
 KW cartilage; cardiac tissue; lung tissue; uterine tissue;
 KW intestinal tissue; vascular tissue; neural tissue.

XX OS Homo sapiens.

XX PN WO2000064944-A1.

XX XX 02-NOV-2000.

XX PD

PF 28-APR-2000; 2000WO-US11612.
 PR 28-APR-1999; 99US-0301808.
 XX (GEMY) GENETICS INST INC.
 XX Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;
 PI Whitters MJ, Wood C;
 XX WPI: 2001-024676/03.
 DR N-PSDB; AAC81416.
 XX Treating or inhibiting tissue fibrosis resulting from infection with
 PT schistosoma and wound healing involves administering interleukin-13 or
 PT interleukin-4 antagonist
 PS Claim 1; Page 76-77; 82pp; English.

XX The invention relates to a method of treating fibrosis in a mammal
 CC by administering an interleukin-13 (IL-13) antagonist or an IL-4
 CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding
 CC chain (IL-13bc; AAB29748; AAB29748) of the IL-13 receptor (IL-13R), or
 CC soluble fragments thereof. The method is useful for treating or
 CC inhibiting the formation of tissue fibrosis resulting from the healing
 CC of a wound, including a surgical incision wound, or from infection with
 CC schistosoma. The method may be used to treat fibrosis in a variety of
 CC tissues, particularly liver tissue, but also skin epidermis, skin
 CC endodermis, muscle, tendon, cartilage, cardiac tissue, pancreatic
 CC tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,
 CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut
 CC tissue. The present sequence represents human IL-13bc.

XX Sequence 380 AA;

Query Match 98.7%; Score 2059; DB 22; Length 380;
 Best Local Similarity 99.7%; Pred. No. 3.5e-193;
 Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLISTTFCCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPPLSLD 60
 Db 1 mafvclaigcllytlsttfgctssdssteikvnpqdfvdpvglylylqwppplsl 60

QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNKGIKIAKHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktititknlyhkgdgdlnkgleakhtllpwqctngse 120

QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
 Db 121 sswaettywispgipetkvdmdcvynwqyllcswkpgigvlltdnynlfywegldh 180

QY 181 ALQCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNVKPLP 240
 Db 181 alqcvdyikadgqngicrfyleasdykdfyicvngsenkpirssyftfqlqnvkplp 240

QY 241 PVIYFTFRESSCEIKLWSIPGLPIPARCFDYIEIRDEDTTLVATVENETYTLKTTNE 300
 Db 241 pviyftfressceiklwsipglpigarcfdyieirddtllvatvenetytlktne 300

QY 301 TRQJCFVVRKVNICYSDDGIWSEWSKQWEGEDLSKTLRLFWLPGFTLILVIFVTG 360
 Db 301 trqlcfvvrskvniycsddgiwsewsdkqwegedlsktlrlfwlpgftlilvifvtg 360

QY 361 LLRKPNTPYKMW 373
 Db 361 llrkpntypkmi 373

RESULT 10
 AAW36614

ID AAW36614 standard; Protein: 380 AA.

XX XX AAW36614;

30-MAR-1998 (first entry)
 Human Zcytor2 cytokine receptor protein.
 Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 infertility; antagonist; contraceptive; diagnostic; therapeutic.
 Homo sapiens.
 WO9733913-A1.
 18-SEP-1997.
 12-MAR-1997; 97WO-US04043.
 13-MAR-1996; 96US-0013345.
 (ZYMO) ZYMOGENETICS INC.
 Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
 O'Hara PJ;
 WPI; 1997-470820/43.
 DR N-PSDB; AAT96783.
 New nucleic acid encoding testis-specific cytokine receptor - useful
 for identification of ligands or antagonists, potentially for use as
 male contraceptives or for infertility treatment
 Claim 1; Page 51-53; 79pp; English.
 This sequence represents a novel ligand-binding receptor, Zcytor2, which
 shares homology with cytokine receptors and was isolated from a human
 testis cDNA library. The resulting polypeptide is a receptor for
 cytokines (particularly interleukin-13) and is expressed on the surface
 of testicular cells, probably being involved in spermatogenesis. It can
 be used to detect ligands that promote proliferation and/or
 differentiation of such cells in cultures and may also be used to treat
 infertility. Antagonists of this receptor may be used to characterise
 ligand-receptor interactions and as male-specific contraceptives. By
 blocking the action of IL-13, receptor antagonists and ligand-binding
 this receptor can also be used to modulate immune function, e.g. in
 allergy and asthma, as a diagnostic to determine circulating levels of
 ligand and also to isolate and purify ligands. Antibodies can be used to
 assay circulating receptor (an abnormal level may be indicative of
 disease such as cancer), for labelling cells that express the receptor,
 and therapeutically as antagonist.
 Sequence 380 AA;

Query Match 97.4%; Score 2033; DB 18; Length 380;
 Best Local Similarity 98.94; Pred. No. 1.2e-190;
 Matches 369; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 1 MAFVCLAIAGCLYTLISTFCTSSDTEIKVNPDPQFEIVDPGVLGYLQWPPPLSLD 60
 1 mafvclaiagclyltlistftgctssdteikvnpdpqfeivdpgylvlylqwpplsl 60
 61 HFKECTVEYELKYNIGSETWTKTITIKNLHYKOGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 61 hfkektveyelkynigsetwtkitknlykdgfdlنگkieakihrlpwqctngsevg 120
 121 SSWAETTYWISPGIPEKTVQDMCVYNNWQYLILCSWKPGIGVLLDNYNLFYWEGLDH 180
 121 sswaettywispgipetkvdmcvynnwqylilcswkpgigvlldtnynlfywegldh 180
 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSGSENKPIRSSYFTFOLQNVKPLP 240
 181 alqcvdykadqngicrfpyleasdykdfyicvngsgsenkpirssyftfqlqnvkplp 240
 241 PVYLTFRESSCEIKLKWISPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTNE 300

Db 241 pvytlftressceiklkwisplgpiiparcfdyeieireddttlvtatvenetytlktne 300
 Qy 301 TROLCFVVRKSVNLYCSDGDTGSEMSDKQWEGEDLSKTLRLRELPFGFTLLILVIFVTG 360
 Db 301 trqlcfvvrskvnlycsddgtgsemsdkqwegedlskttlrlrfwlpfgftllilvifvtg 360
 Qy 361 LLLRKPNNTYPKMV 373
 Db 361 lllrkpnntypkmi 373
 RESULT 11
 AAW36616
 ID AAW36616 standard; Protein; 372 AA.
 AC AAW36616;
 DT 30-MAR-1998 (first entry)
 DE Celebus macaque Zcytor2 protein.
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
 OS Macaque sp.
 FH Key Location/Qualifiers
 FT Protein i..372
 FT /label= zcytor2
 FT /note= "partial protein sequence"
 XX WO9733913-A1.
 XX 18-SEP-1997.
 XX 12-MAR-1997; 97WO-US04043.
 XX 13-MAR-1996; 96US-0013345.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
 PI O'Hara PJ;
 WPI; 1997-470820/43.
 DR N-PSDB; AAT96784.
 New nucleic acid encoding testis-specific cytokine receptor - useful
 for identification of ligands or antagonists, potentially for use as
 male contraceptives or for infertility treatment
 Example 4; Page 56-57; 79pp; English.
 This sequence represents a novel ligand-binding receptor, Zcytor2,
 which shares homology with cytokine receptors and is isolated from
 testis tissue obtained from a Celebus macaque. The resulting polypeptide
 is a receptor for cytokines (particularly interleukin-13) and is
 expressed on the surface of testicular cells, probably being involved in
 spermatogenesis. It can be used to detect ligands promoting proliferation
 and/or differentiation of such cells in cultures and may also be used to
 treat infertility. Antagonists of this receptor may be used to
 characterise ligand-receptor interactions and as male-specific
 contraceptives. By blocking the action of IL-13, receptor antagonists and
 ligand-binding this receptor can also be used to modulate immune
 function, e.g. in allergy and asthma, as a diagnostic to determine
 circulating levels of ligand and also to isolate and purify ligands.
 Antibodies can be used to assay circulating receptor (an abnormal level
 may be indicative of disease such as cancer), for labelling cells that
 express the receptor, and therapeutically as antagonist.
 Sequence 372 AA;

Query Match 88.8%; Score 1853; DB 18; Length 372;
Best Local Similarity 92.2%; Pred. No. 5e-173;
Matches 343; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTFLLSTTFCGTSSTSDTEIKVNPQDPFVIDPGYLGLYLQWQPPLSLD 60
DB 1 mafvylairclctflsttfgytstsdteikvnpqdpfvidpgylglYLQWQPPLSLD 60

QY 61 HPKECTVEYELKYRNGISGTSWKTITTKNLHYKDGFDLNGKIEAKHTLLPWQCTNGSEVQ 120
DB 61 nKectveYelkyrNgisGtsWktITTKnlHyKdgfdLnGkIeakhtllpWqctngseVq 120

QY 121 SSWAETTWISPGQIPERKVDMDCVYINWQYLLCSWRPGIGVLLDTNINLFYWYEGLDH 180
DB 121 sswaEttWiSpGqIpErKvDmDcVyiNwQyLlCsWrpGigVllDtnInLfYwYegldH 180

QY 181 ALQCVDYIKADQNTGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQQLNTVKPLP 240
DB 181 alqcvdyIkAdQnTGcRfPyleASdyKdFYiCvNgSSeNkPiRSsYtFqQLnTvKPlP 240

QY 241 PVLFTTRESSCEIKLWSIPLGPPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE 300
DB 241 pvlctctgesYelkLwSiPlGpPiPaRcfDYeIeIrEdDttLvtAtVeNeTyTLkTtNe 300

QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQCEGEGEDLSKKTLLRFLPFGFILLVIFVTG 360
DB 301 trqlcfvvrKvnIcYsDgDiWseWskQceGegEdLSkKtLLrFlPfgFiLLvIfvtG 360

QY 361 LLLRKPNTYPKM 372
DB 361 lllckrdsypkm 372

RESULT 12
AAW56261
ID AAW56261 standard; Protein; 315 AA.
XX
AC AAW56261;
XX
DT 16-SEP-1998 (first entry)
XX
DE Mature interleukin-13 binding protein.
XX
KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.
XX
OS Homo sapiens.
XX
PN WO9810638-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-AU00591.
XX
PR 27-FEB-1997; 97AU-0005374.
XX
PR 10-SEP-1996; 96AU-0002262.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX
DR WPI; 1998-207062/18.
XX
DR N-PSDB; AAV22702.
XX
PT New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX
PS Disclosure; Page 55-56; 69pp; English.
XX
CC The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for

CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX
SQ Sequence 315 AA;

Query Match 84.0%; Score 1753; DB 19; Length 315;
Best Local Similarity 100.0%; Pred. No. 2.4e-163;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPQDPFVIDPGYLGLYLQWQPPLSLDHFKECTVEYELKYRNGISGTSWKTITTKN 88
DB 1 eikvnpqdpfvidpgylglYLQWQPPLSLdHfKectveYelkyrNgisGtsWktIttkN 88

QY 89 LHYKDGFDLNGKIEAKHTLLPWQCTNGSEVQSSWAETTWISPGIPETKVQDMDCVY 148
DB 61 lhyKdgfdLnGkIeakhtllpWqctngseVqssWaeTtwiSpGIpEtKvQdmDcVyy 120

QY 149 NWQYLLCSWKPGIGVLLDTNINLFYWYEGLDHALQCVDYIKADGONICRFPYLEASDYK 208
DB 121 nwqyLlCsWkPgigVllDtnInLfYwYegldHalqcvDYiKadGonIcRfPyleasdyK 180

QY 209 DFYICVNGSSSENKPIRSSYTFQQLNTVKPLPPVYLTFTRESSCEIKLWSIPLGPPIPAR 268
DB 181 dfyIcVngSSeNkPiRSsYtFqQLnTvKPlPpVylTfTressceIkLwSiPlGpPiPaR 240

QY 269 CFDEIEIREDDTTLVTATVENETYTLKTTNETROLCFVVRKVNICYSDGDIWSEWSK 328
DB 241 cfDeIeIrEdDttLvtAtVeNeTyTLkTtNeTrqlcfvvrKvnIcYsDgdiWseWsdK 300

QY 329 QCWEGEDLSKKTLLR 343
DB 301 qcweGedlSkKtllr 315

RESULT 13
AAW56260
ID AAW56260 standard; Protein; 359 AA.
XX
AC AAW56260;
XX
DT 16-SEP-1998 (first entry)
XX
DE Construct containing mature interleukin-13 binding protein.
XX
KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.
XX
OS Homo sapiens.
XX
PN WO9810638-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-AU00591.
XX
PR 27-FEB-1997; 97AU-0005374.
XX
PR 10-SEP-1996; 96AU-0002262.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX
DR WPI; 1998-207062/18.
XX
DR N-PSDB; AAV22701.
XX
PT New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX

Example 14; Page 52-53; 69pp; English.

PS The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX
SQ Sequence 359 AA;

Query Match 84.0%; Score 1753; DB 19; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.9e-163;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 EIKVNPQDFEIVDPGYLYLQWQPLSLDHPKCEVYELKYRNIGSETWTKITIKN 88
Db 45 eikvnpqdfelvdpgylylqwpplslldhfkectveylkynrgisgsetwtkitickn 104
QY 89 LHYKDFDLNGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCVY 148
Db 105 lhykdfdlngieakihltllpwqctngsevgsswaettywispqgipetkvqdmdevy 164
QY 149 NWQYLLCSWKPGIGVLLDTNLFYWEGLDHALQCVDIKADGONIGCRPPYLEASDYK 208
Db 165 nwqyllcswkpgigvlltdnlnfywyegldhalqcvdyikadgnigcrfpyleasydk 224
QY 209 DFYICVNGSSNKPIRSSYFTFQONIVKPLPPVYLTFTRESSCEIKLWSIPGIPAR 268
Db 225 dfyicvngssenkpirssyftfqlnkvkplppvytftressceiklwsipgipar 284
QY 269 CFDEYIEITREDTTLVATVENETLTNTETCOLCFVBSKNVYCSDDGIWSESDK 328
Db 285 cfdeyieitredtltvatvenetyltkntetrcqlcfvbskrnvlycsddgiwsewskd 344
QY 329 QCWEGEDLSKTKLLR 343
Db 345 qcwegedlskttllr 359

RESULT 14
AAW35294
ID AAW35294 standard; Protein; 383 AA.

AC AAW35294;

XX 27-MAR-1998 (first entry)

DE Murine IL-13 binding chain of the IL-13 receptor.

KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
KW allergy; asthma; immune complex disorder.

XX Mus sp.

XX Key Location/Qualifiers

FT Peptide

FT /label= signal_sequence

FT /note= "putative"

FT 22..383

FT Protein

FT /label= mature_protein

FT 22..334

FT /label= extracellular_domain

FT 335..356

FT /label= transmembrane_domain

FT 357..383

FT /label= intracellular_domain

XX W09731946-A1.

PD 04-SEP-1997.

XX 28-FEB-1997; 97WO-US03124.

XX 01-MAR-1996; 96US-0609572.

XX (GEMY) GENETICS INST INC.

PA Collins M, Donaldson D, Fitz L, Neben T, Whitters M;

PI Wood C;

XX WPI; 1997-448632/41.

DR N-PSDB; AAT75213.

XX New nucleic acid encoding interleukin-13 receptor binding chain and

PT transformed cells - proteins, antibodies and inhibitors, for

PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,

PT and in diagnosis

XX Claim 11; Pages 30-31; 49pp; English.

XX The present sequence represents the murine interleukin-13 (IL-13) binding

CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a

CC mediator of the known biological activities of IL-13. Recombinant

CC IL-13bc proteins, and antibodies raised against them, are used to

CC inhibit the binding of IL-13 to its receptor. They are particularly used

CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex

CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.

CC They are also used to treat immune deficiency (particularly in

CC haematopoietic progenitor cells), cancer etc., and to increase macrophage

CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein

CC with such activity is combined with IL-13bc and the mixture applied,

CC in vivo, to a cell expressing at least one chain of the IL-13 receptor

CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect

CC expression of IL-13, its receptor or binding chain, and to raise specific

CC antibodies which may be useful for treating some tumours.

XX Sequence 383 AA;

Query Match 57.2%; Score 1194.5; DB 18; Length 383;

Best Local Similarity 58.9%; Pred. No. 1.4e-108;

Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

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Db 1 mafv--hircclfcilctitgys----leakvnpqdfellpdlpdllylylqwkppvvie 54

QY 61 HFKECTVEYELKYRNIGSETWTKITITKNLHYKDGFDLNGIEAKIHTLLPWQCTNGSEVQ 120

Db 55 kfgctleyelkyrnvdswkttitnrllykdgfdlنگiegkirthlsehtngsevg 114

QY 121 SSWAEFTYWTSPQIPETKVQDMDCVYNNWQYLLCSWKPGIGVLLDTNLFYWEGLDH 180

Db 115 spwleasygisdegslctkqdmkciyynwqylvcswkpgktvysdntnftffvegldh 174

QY 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSNKPIRSSYFTFQONIVKPLP 240

Db 175 alqcadyldqdeknvgcklsnldssdykdfcivngsskilepirssyvtvqlnkvplp 234

QY 241 PVYLTFTRESSCEIKLWSIPGIPARCFDYETIEIRDDFTLTVATVENETYLTKTNE 300

Db 235 peflhisvensidirmkwstpggipprcycyeylveirddiswesatdkndmkkrane 294

QY 301 TROLCFVVRKSNVLYCSDDGIWSEMSDKQWEGEDLSKTKLLRFLWLPFGFTLLILVIFVTG 360

Db 295 sedlcfvvrkvnlycsaddgiwsewseeecwgytgpdkii-fivpvcilffillilic 353

QY 361 LLRLKPNTPK 372

Db 354 livekeepetl 365

CONFIDENTIAL

Search completed: September 1, 2001, 19:17:23
Job time: 30 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:53 ; Search time 12.28 Seconds
(without alignments)
633.807 Million cell updates/sec

Title: US-09-077-817-12
Perfect score: 2087
Sequence: 1 MAFVCLAIGCLYFLISTTF.....TGILLRKPNYPKMYRCVTL 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2059	98.7	380	1	US-08-609-572-4
2	2059	98.7	380	4	US-08-841-751-4
3	2059	98.7	380	4	US-08-846-340-4
4	1194.5	57.2	383	1	US-08-609-572-2
5	1194.5	57.2	383	4	US-08-841-751-2
6	1194.5	57.2	383	4	US-08-846-340-2
7	310.5	14.9	420	1	US-07-757-390-13
8	310.5	14.9	420	1	US-08-442-281-13
9	310.5	14.9	420	1	US-08-442-281-13
10	310.5	14.9	420	2	US-08-939-727-13
11	309.5	14.8	396	1	US-07-757-390-14
12	309.5	14.8	396	1	US-08-442-282-14
13	309.5	14.8	396	1	US-08-442-281-14
14	309.5	14.8	396	2	US-08-939-727-14
15	294.5	14.1	427	4	US-08-969-125-9
16	293	14.0	313	3	US-08-836-561-106
17	292	14.0	335	1	US-07-947-130-2
18	292	14.0	335	1	US-08-421-822-2
19	292	14.0	335	1	US-08-421-823-2
20	241	11.5	398	1	US-07-757-390-6
21	241	11.5	398	1	US-08-442-282-6
22	241	11.5	398	1	US-08-442-281-6
23	241	11.5	398	2	US-08-939-727-6
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27	241	11.5	415	2	US-08-939-727-5

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29	229	11.0	315	1	US-08-442-282-8	Sequence 8, Appli
30	229	11.0	315	1	US-08-442-281-8	Sequence 8, Appli
31	229	11.0	315	2	US-08-939-727-8	Sequence 7, Appli
32	229	11.0	332	1	US-07-757-390-7	Sequence 8, Appli
33	229	11.0	332	1	US-08-442-282-7	Sequence 7, Appli
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37	229	11.0	335	1	US-08-421-822-3	Sequence 3, Appli
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41	219	10.5	347	1	US-08-052-205-7	Sequence 7, Appli
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43	212.5	10.2	369	2	US-08-424-224-2	Sequence 2, Appli
44	212.5	10.2	369	5	PCT-US94-02891-69	Sequence 69, Appli
45	207	9.9	252	1	US-08-052-205-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-609-572-4
; Sequence 4, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-609-572-4

Query Match 98.7% Score 2059; DB 1: Length 380;
Best Local Similarity 99.7%; Pred. No. 2.1e-203;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYFLISTTFCTSSDTEIKVNPQDPFIVDPGYLYLQWQPLSLD 60

Db 1 MAFVCLAIGCLYTLSTTFTGCTSSSDTEIKVNPDPQFEIVDPGYLGLYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
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Qy 241 PVLTFTRSSCEIKLWSPILGPIPARCFDYEIEIREDDDTTLVATVAVENETYLKTTNE 300
Db 241 PVLTFTRSSCEIKLWSPILGPIPARCFDYEIEIREDDDTTLVATVAVENETYLKTTNE 300
Qy 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGEDLSKTKTLRLFWLPGFGLILVIFVTG 360
Db 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGEDLSKTKTLRLFWLPGFGLILVIFVTG 360
Qy 361 LLLRKPNTYPRKMV 373
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RESULT 2

US-08-841-751-4
; Sequence 4, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-841-751-4

Query Match 98.7%; Score 2059; DB 4; Length 380;
Best Local Similarity 99.7%; Pred. No. 2.1e-203;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLSTTFTGCTSSSDTEIKVNPDPQFEIVDPGYLGLYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTLSTTFTGCTSSSDTEIKVNPDPQFEIVDPGYLGLYLQWQPPLSLD 60
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Qy 241 PVLTFTRSSCEIKLWSPILGPIPARCFDYEIEIREDDDTTLVATVAVENETYLKTTNE 300
Db 241 PVLTFTRSSCEIKLWSPILGPIPARCFDYEIEIREDDDTTLVATVAVENETYLKTTNE 300
Qy 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGEDLSKTKTLRLFWLPGFGLILVIFVTG 360
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RESULT 3

US-08-846-340-4
; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-4

Query Match 98.7%; Score 2059; DB 4; Length 380;
Best Local Similarity 99.7%; Pred. No. 2.1e-203;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAFVCLAIGCLYTLFTISCTSSDTEIKVNPQDPEIVDPGVLYLQWQPPLSLD 60
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RESULT 4
US-08-609-572-2
Sequence 2, Application US/08609572
Patent No. 5710023

GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,572
FILING DATE:
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-572-2

Query Match 57.2%; Score 1194.5; DB 1; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.6e-114;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

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DB 55 KFKGCTLEVELKYRNVSDSNKTIITRNLIVKDGFDLNGKIEGKIRTHLSHCCTNGSEVQ 114
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DB 115 SPWIEASVIGSDEGSLETKIQDMKCIYYNNQYLLCSWKPGLDNTNLYFYWYEGLDH 174
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DB 175 ALQCADYIQLHDEKKNVCKLSNLDSDYKDFYICVNGSSSKLEPIRSSYTFOLQNVKPLP 234
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DB 235 PEFLLHISVENSIDIRMKWSTPGGPPIPRCYTYEIVIREDDISWESATDKNDMKLKRANE 294
QY 301 TRQLCFVVRKVNICYSDDGWSESDKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
DB 295 SEDLCFFVRCVKVNICYCADDGIWSESEECWEGYTGTPDSKII-FIVPVCPLFFILLLLC 353
QY 361 LLRRKPNTYPKM 372
DB 354 LIVEKEEPEPTL 365
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RESULT 5
US-08-841-751-2
Sequence 2, Application US/08841751
Patent No. 6214559
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/841,751
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-841-751-2

Query Match 57.2%; Score 1194.5; DB 4; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.6e-114;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLATGCLYTLISTFGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPPLSLD 60
DB 1 MAFV-HIRCLCFILLCTITGYS----LEIKVNPQDFEILDGGLGYLYLOWPPVIVIE 54
QY 61 HFKECTVEYELKYNIGSEWTKTITRNLYKDGFDLNGKIEAKHTLHPQCTNGSEVQ 120
DB 55 KFGCTLEYELKYNVDSWTKTITRNLYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114
QY 121 SSWAETTYWISPOGIPETKVDMDCVVYNNQYLLCSWKPGLVLDNTNLYFYWYEGLDH 180
DB 115 SPWIEASGIDEGSLETKIQDMKCIYNNQYLLCSWKPGLVSDNTNLYFYWYEGLDH 174
QY 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSENKPIRSSYTFQLOQIVKPLP 240
DB 175 ALQCADYLQHDEKKNVCKLSNLDSSDYKDFYICVNGSKLEPIRSSYTFVQLOQIVKPLP 234
QY 241 PVYLTFRESSECEIKLWSIPGLPIPARCFDYETIREDDTTLVATVENTYTLKTTNE 300
DB 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDMKLRRANE 294
QY 301 TROLCFVVRKVNICYSDGDIWSEMSDKQWEGEDLSKKTLLRFLWLPFGFLLILVIFVTG 360
DB 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEGYTGPDSKII-FIVPVCLEFFIFLLILLC 353
QY 361 LLRLKPNYTPKM 372
DB 354 LIVEKEPEPTL 365

RESULT 6
US-08-846-340-2
Sequence 2, Application US/08846340
Patent No. 6248714
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whittiers, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/846,340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-2

Query Match 57.2%; Score 1194.5; DB 4; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.6e-114;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLATGCLYTLISTFGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPPLSLD 60
DB 1 MAFV-HIRCLCFILLCTITGYS----LEIKVNPQDFEILDGGLGYLYLOWPPVIVIE 54
QY 61 HFKECTVEYELKYNIGSEWTKTITRNLYKDGFDLNGKIEAKHTLHPQCTNGSEVQ 120
DB 55 KFGCTLEYELKYNVDSWTKTITRNLYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114
QY 121 SSWAETTYWISPOGIPETKVDMDCVVYNNQYLLCSWKPGLVLDNTNLYFYWYEGLDH 180
DB 115 SPWIEASGIDEGSLETKIQDMKCIYNNQYLLCSWKPGLVSDNTNLYFYWYEGLDH 174
QY 181 ALQCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSENKPIRSSYTFQLOQIVKPLP 240
DB 175 ALQCADYLQHDEKKNVCKLSNLDSSDYKDFYICVNGSKLEPIRSSYTFVQLOQIVKPLP 234
QY 241 PVYLTFRESSECEIKLWSIPGLPIPARCFDYETIREDDTTLVATVENTYTLKTTNE 300
DB 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDMKLRRANE 294
QY 301 TROLCFVVRKVNICYSDGDIWSEMSDKQWEGEDLSKKTLLRFLWLPFGFLLILVIFVTG 360
DB 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEGYTGPDSKII-FIVPVCLEFFIFLLILLC 353
QY 361 LLRLKPNYTPKM 372
DB 354 LIVEKEPEPTL 365

RESULT 7
US-07-757-390-13
Sequence 13, Application US/07757390
Patent No. 5453491
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tomimaga, Akira
APPLICANT: Takagi, Satoshi

```

; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-757-390-13

```

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Query Match      14.98; Score 310.5; DB 1; Length 420;
Best Local Similarity 27.9%; Pred. No. 1.3e-23;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;

```

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QY 27 DTEIKVNPQDFEIVDPGLGYLQWOPPLSLDHFKECTVEYELKYRNIGSETWTKTIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DEKISLLPPVNFTHKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 87 KNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVSSWAETTYWISPOGIPETKYQDMDCV 146
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAELH-APPGSPGTSVNNLTCT 135
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNNTNLFY---WYEGLDHALQCVDYIKAD 191
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TMTTNDNYSLRYSQVSLHCTWLVTGTDAPEDTQVFLYRYGSWTE-----ECOYEYSDT 189
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLNIVKPLPPVLTFT 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACWFPFTILSKGRDLAVLVNGSSKSAIRPFDQLFALHAIDQINPLNVTAEI 249
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 249 ESSCEIKLWSIPLGIPARCFDYEIEIREDDTTLVTATVENETTYLTKTNETRQLCFV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWEKPVSAPIHCFDYEIVKTHNRNGYLOIEKLTWNAFISIDDLKSYDVQV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 309 RSKVNIYCSDDGINSWSDKOCWEGEDLSKTLRLFWLPFGFILLVIFVNGLL 363
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSSMCREAGLWSEWS-QPIYYVGNDEHKP--LREW----FVIVIMATICFILL 356
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

RESULT 8
US-08-442-282-13
; Sequence 13, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira

```

```

; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-282-13

```

```

Query Match      14.98; Score 310.5; DB 1; Length 420;
Best Local Similarity 27.9%; Pred. No. 1.3e-23;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;

```

```

QY 27 DTEIKVNPQDFEIVDPGLGYLQWOPPLSLDHFKECTVEYELKYRNIGSETWTKTIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DEKISLLPPVNFTHKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 87 KNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVSSWAETTYWISPOGIPETKYQDMDCV 146
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAELH-APPGSPGTSVNNLTCT 135
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNNTNLFY---WYEGLDHALQCVDYIKAD 191
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TMTTNDNYSLRYSQVSLHCTWLVTGTDAPEDTQVFLYRYGSWTE-----ECOYEYSDT 189
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLNIVKPLPPVLTFT 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACWFPFTILSKGRDLAVLVNGSSKSAIRPFDQLFALHAIDQINPLNVTAEI 249
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 249 ESSCEIKLWSIPLGIPARCFDYEIEIREDDTTLVTATVENETTYLTKTNETRQLCFV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWEKPVSAPIHCFDYEIVKTHNRNGYLOIEKLTWNAFISIDDLKSYDVQV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 309 RSKVNIYCSDDGINSWSDKOCWEGEDLSKTLRLFWLPFGFILLVIFVNGLL 363
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSSMCREAGLWSEWS-QPIYYVGNDEHKP--LREW----FVIVIMATICFILL 356
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

RESULT 9
US-08-442-281-13
; Sequence 13, Application US/08442281

```

```

: Patent No. 5807991
:
: GENERAL INFORMATION:
:
: APPLICANT: Takatsu, Kiyoshi
: APPLICANT: Tomimaga, Akira
: APPLICANT: Takagi, Satoshi
: APPLICANT: Murata, Yoshiyuki
: TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/442,281
: FILING DATE:
:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/757,390
: FILING DATE: 10-SEP-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Misrock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 7005-030
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 8698864/9741
: TELEX: 66141 PENNIE
:
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 420 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
:
: US-08-442-281-13

```

```

Query Match      14.9%; Score 310.5; DB 1; Length 420;
Best Local Similarity 27.9%; Pred. No. 1.3e-23;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;

QY 27 DTEIKVNPQDFEIVDPGYLGYLQWQPPPLSLDHFRECTEYELKYNIGSEWTKTIIT 86
   | : | : | | | | | : | | | : | : | : | : | : | : | : | : |
Db 25 DEKISLPPVNFITKVTG-LAQVLLQWKPNPDQ80-RNVNLEYQVKINAPKEDDYETRI 82
   : : | : | | | : | : | : | : | : | : | : | : | : | : | : |
QY 87 KNLHYKDGDFOLNKIEAKIHTLLPQWCTNGSEVGSSWAETTYTWISPOGIPKTKVQDMDCV 146
   : : | : | | | : | : | : | : | : | : | : | : | : | : | : |
Db 83 ES---KCVTILHKGFSASVRTILQ---NDHSLASSWASAEHL-APPGSPGTSVNLNCT 135
   : : | : | | | : | : | : | : | : | : | : | : | : | : | : |
QY 147 -----YYNQYLL-CSWKPGIGVLLDTNYNLPY----WYEGLDHALQCVDYIKAD 191
   | : | : | | | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TTTTETDNYSLRSLYQVSLHCTWLVTGTDAPETQYFLYYRGSWTE-----ECQEYSKDT 189
   : : | : | | | : | : | : | : | : | : | : | : | : | : | : |
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLQNIKVPPLPYVLTFR 248
   | : | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACWFRTFTLSKGRDWLAVLVNGSSKHSIAIRFPDQLFALHAIDQINPPLNVTAEI 249
   : : | : | | | : | : | : | : | : | : | : | : | : | : | : |
QY 249 ESSEIKLKWSPIDPLGPAPRCDFYIEIERDDTTLVTATVENETYTLKTTETROLCFW 308
   | : | : | | | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWEKPPSAFPHCFDFYEVKIHTRNGYIQIEKLMTNFAFISIIDLKDYQVQ 308
   | : | : | | | : | : | : | : | : | : | : | : | : | : | : |
QY 309 RSKVNIYCSDDGIWSEWSDKOCWEGEDLSKTLRFLWLPFGFILIILVFTVGLLL 363
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLI 356
   : : | : | | | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 10
 US-08-939-727-13
 : Sequence 13, Application US/08939727
 : Patent No. 5916767
 : GENERAL INFORMATION:
 : APPLICANT: Takatsu, Kiyoshi
 : APPLICANT: Tominaga, Akira
 : APPLICANT: Takagi, Satoshi
 : APPLICANT: Murata, Yoshiyuki
 : TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pennie & Edmonds
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 10036-2711
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION NUMBER: US/08/939, 727
 : APPLICATION DATA:
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/757,390
 : FILING DATE: 10-SEP-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Misrock, S. Leslie
 : REGISTRATION NUMBER: 18,872
 : REFERENCE/DOCKET NUMBER: 7005-030
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 212 790-9090
 : TELEFAX: 212 8698864/9741
 : TELEX: 66141 PENNIE
 : INFORMATION FOR SEQ ID NO: 13:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 420 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: unknown
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 :

Query Match	14.9%;	Score	310.5;	DB	2;	Length	420;
Best Local Similarity	27.9%;	Pred. No.	1.3e-23;				
Matches	99;	Conservative	64;	Mismatches	151;	Indels	41;
Gaps							
Qy	27	DTEIKVNPDPQFEIVDPGYLGYLVLQWQPPSLDHFKECTVVELYKYNIGSTWTKTIT	86				
Db	25	DEKISLLPPVNTFKVVG-LAQVLLQWKPNPQDEQ-RNVNLEYQVKINAPKEDDYETRI	82				
Qy	87	KNLHYKQGFDLNKGIEAKIHTLLPWCQTCNSEVQSSNAETTYWISQGPETKTVQDMDCV	146				
Db	83	ES-----KCVTILHKGFSAVRTILQ-----NDHSLASSWASAEHL-APPGSGTSVNLCT	135				
Qy	147	-----YNNQYLL-CSWPKGIGVLDDTNLIFY-----WEGLDHALQCVDIKAD	191				
Db	136	TNTTDDNYSRLRSQVSLHCTWLVTGTDAPETQFLYYRGSWTE-----ECQEFYSKT	189				
Qy	192	-GQNGICRFP--YLEASDYKDFYICVNGSENKPIRSSYTFQLOINIVKPLPVLFTFR	248				
Db	190	LGRNIACWFPTFILSKGROWLAVLVNGSSKHSARFPDQIFALHAIDQINPLNVTAEI	249				
Qy	249	ESSECIKLKWSIPGPIPARCFDYEIEIREDDTFLVTATVVENETYTLKTTNETRQJCFVV	308				
Db	250	EGT--RLSTQWKPPYSAPPIHCFDFEVKIHNRNGYLQIEKLMFNAFISIIDLSKSYDVQV	308				

Qy 309 RSKVNIYCDGDIWSEWSKOCWEGEDLSKTKLLRFWLPFGFILLILVIFVGTGLL 363
 Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILL 356

RESULT 11

US-07-757-390-14
 ; Sequence 14, Application US/07757390
 ; Patent No. 5453491
 ; GENERAL INFORMATION:
 ; APPLICANT: Takatsu, Kiyoshi
 ; APPLICANT: Tominaga, Akira
 ; APPLICANT: Takagi, Satoshi
 ; APPLICANT: Murata, Yoshiyuki
 ; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07757,390
 ; FILING DATE: 19910910
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7005-030
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEFAX: 212 8698864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 396 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-07-757-390-14

Query Match 14.8%; Score 309.5; DB 1; Length 396;
 Best Local Similarity 27.6%; Pred. No. 1.6e-23;
 Matches 98; Conservative 65; Mismatches 151; Indels 41; Gaps 15;

Qy 27 DTEIKVNPDPQFEIVDPGLYLYLOWOPPLSLDFHFKCTVEYELKYRNIGSETWKTIIIT 86
 Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
 Qy 87 KNLHYKDFGLNKGEAKIHTLLPWQCTNGSEVSSWAETTYWISPOGIPETKVQDMDCV 146
 Db 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAEHL-APPGSPGTSIVNLTC 135
 Qy 147 -----YNNQYLL-CSWKKPGIGVLLDTNLYFY---WYEGDLHALQCVDYIKAD 191
 Db 136 TMTEDNYSRLRSQVSLHCTWLVGTDAPEDTQFLIYRYGSWTE-----ECQEYSKDT 189
 Qy 192 -GONIGCRFP--YLEASDYKDFICVNGSSSENKPIRSSYFTFQLNIVKPLPPVLTFT 248
 Db 190 LGRNIACWFPRTFILSKGRDLAVLVNGSSKHSAIRPPDQLFALHAIDQINPPLNVTAEI 249
 Qy 249 ESSCEIKLWSIPGLPIPARCFDEIIEIREDDTLVATVENEYITLKTWNETQLCFV 308
 Db 250 EGT-RLSIQWKEKPVSAFPIHCFDYEKVIHNRNGYLQTEKLTNAFISIIDLSKYDVQV 308

Qy 309 RSKVNIYCDGDIWSEWSKOCWEGEDLSKTKLLRFWLPFGFILLILVIFVGTGLL 363
 Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILL 356

RESULT 12

US-08-442-282-14
 ; Sequence 14, Application US/08442282
 ; Patent No. 5760204
 ; GENERAL INFORMATION:
 ; APPLICANT: Takatsu, Kiyoshi
 ; APPLICANT: Tominaga, Akira
 ; APPLICANT: Takagi, Satoshi
 ; APPLICANT: Murata, Yoshiyuki
 ; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08442,282
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/757,390
 ; FILING DATE: 10-SEP-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7005-030
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEFAX: 212 8698864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 396 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-442-282-14

Query Match 14.8%; Score 309.5; DB 1; Length 396;
 Best Local Similarity 27.6%; Pred. No. 1.6e-23;
 Matches 98; Conservative 65; Mismatches 151; Indels 41; Gaps 15;

Qy 27 DTEIKVNPDPQFEIVDPGLYLYLOWOPPLSLDFHFKCTVEYELKYRNIGSETWKTIIIT 86
 Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
 Qy 87 KNLHYKDFGLNKGEAKIHTLLPWQCTNGSEVSSWAETTYWISPOGIPETKVQDMDCV 146
 Db 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAEHL-APPGSPGTSIVNLTC 135
 Qy 147 -----YNNQYLL-CSWKKPGIGVLLDTNLYFY---WYEGDLHALQCVDYIKAD 191
 Db 136 TMTEDNYSRLRSQVSLHCTWLVGTDAPEDTQFLIYRYGSWTE-----ECQEYSKDT 189
 Qy 192 -GONIGCRFP--YLEASDYKDFICVNGSSSENKPIRSSYFTFQLNIVKPLPPVLTFT 248
 Db 190 LGRNIACWFPRTFILSKGRDLAVLVNGSSKHSAIRPPDQLFALHAIDQINPPLNVTAEI 249

[illegible]

RESULT 14
US-08-939-727-14
Sequence 14, Application US/08939727
Patent No. 5916767
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,727
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-939-727-14

Query Match	14.8%;	Score 309.5;	DB 2;	Length 396;
Best Local Similarity	27.6%;	Pred. No. 1.6e-23;		
Matches	98;	Conservative	65;	Mismatches 151;
				Indels 41;
				Gaps

QY	27	DT	EIKVNPQD	F	IVDPG	YIGYLYLQW	PP	LSLDH	P	KECTVEY	VELKYRNIG	SETWKT	IT	86
			:	:	:	:	:	:	:	:	:	:	:	
Db	25	DE	KISLLP	PNV	FTIK	VTG-LAQ	VLLQW	K	PNQEQ-RNV	LYEQV	KINAK	PEDD	YETR	82
			:	:	:	:	:	:	:	:	:	:	:	
QY	87	KN	LHYKDG	FD	LNRG	IEAK	ITHTLLP	WQCT	NGSE	VSQSWAET	TYWIS	POGIPET	KVQDMCV	146
			:	:	:	:	:	:	:	:	:	:	:	
Db	83	ES	---	KCV	ITLHK	GFASV	RTILO---	NDS	LLAS	WSAELH-	APPGSPG	TSIVNLTCT	135	

Qy 147 -----YNNQYLL-CSWKPGIGVLLDTNYNLFY----WYEGDLHALQCVDIKAD 191
Db 136 TTTEDNYSRLRSYQVSLHCTWLGTDAPETQVFLYRYGSWTE-----ECQEYSKDT 189
Qy 192 -GONIGCRFP--YLBASYKDFYICVNGSSSENKPIRSSYFTFQLNIVKPLPPVLTETR 248
Db 190 LGRNIACWFPRTFILSKGRDLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI 249
Qy 249 ESSCEIKLWSIPGLPIPARCFDYEIEIREDDTTLVATVENEYTLKTTNETRQLCFVV 308
Db 250 EGT-RLSQWKEKPSAFPHCFDVEVKLHNTRNGVLOEKLMTNAFISIIDLSKYDVQV 308
Qy 309 RSKVNIYCSDDGIMSEWSKOCWEGEDLSKTKLLRFLWLPFGFILILVIFVTGLLL 363
Db 309 RAAVSSMCREAGLSEWS-QPIYVGNDEHKP--LREW---FVIVIMATICFILL 356

RESULT 15

US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871

GENERAL INFORMATION:

APPLICANT: BONNEFOY, JEAN-YVES
GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR USES

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.

ZIP: 22201-4714

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/969.125B

FILING DATE: 12-No. 6143871-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9625899.1

FILING DATE: 13-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955

REFERENCE/DOCKET NUMBER: 1430-179

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4000

TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 427 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-08-969-125-9

Query Match 14.1%; Score 294.5; DB 4; Length 427;
Best Local Similarity 26.3%; Pred. No. 6.1e-22;
Matches 101; Conservative 59; Mismatches 161; Indels 63; Gaps 18;

Qy 11 LYTFLLISTFCTSSDPEIKVNPQDFEIVDPGYLYLQWQPPLSLDHFKECTWEY- 69

Db 10 LWALLCAGGGGGGAAPTQPPVNLVSVENLCTVIWVWNPPEGAS--SNCSLWYF 67

Qy 70 ----ELKYRNTGSETWTKTITTKNLNHYKDGFDLNGIEAKIHTLLPWQC--TNGSEVQSSWA 124

Db 68 SHFGDKQDKKIAPETRRSI-----EVPLNERICLVGVS-----QCSTNESEKPSILV 114
Qy 125 ETTYWIS-POGIPETKYODMDCVYVYNWQYLLCSWKPGIGVLLDTNYNLFYXWEGDLHALQ 183
Db 115 EKC--ISPPEGDPESAVTELOCIWHNLSTMKCSWLPGRNTSPDNTYTLYYWHRSLKTIHQ 172
Qy 184 CVDYIKADGQNGICRFPYLEASD--YKDFYICVNGSSSENKPIRSSYFTFQLNIVKPLPP 241
Db 173 C-ENIFREGQYFGCSFDLTVKVDSFQHSQVIMVKDNAGKIKPSFNIVPLTSRVKPPDP 231
Qy 242 --VILFTTRESSCEIKLWKSIPGLPIPARCFDYEIEIREDDTT-----LYTATVENTY 293
Db 232 HIKNLSFHND---DLVYQWENPQNF1-SRCLFYEYEVVNNSTETHNVFYVQEAECENPEF 287
Qy 294 TLKTTNETRQLCFVV-----RSKVN1YC-SDDG1WSEWSKOCWEGEDLSKK 339
Db 288 ERNVENTS---CFWPGVLPDTLNTVIRVIRVTKLCYEDDKLWSNNSQEM-----SIGKK 339
Qy 340 TLLRFLWLPFGFILILVIFVTGLLL 363
Db 340 RNSTLYIT--MLLIVPVIVAGAI 361

Search completed: September 1, 2001, 19:17:42
Job time: 49 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:24 ; Search time 24.79 seconds
(without alignments)
514.040 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_372
Perfect score: 2056
Sequence: 1 MAFVCLAIGCLYFLISTTF.....ILVIFVTGLLRKPNTPK 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2056	100.0	380	I132_HUMAN	Q14627 homo sapien
2	309.5	15.1	420	I15R_HUMAN	Q01344 homo sapien
3	294.5	14.3	424	I131_MOUSE	O09030 mus musculus
4	294.5	14.3	427	I131_HUMAN	P78552 homo sapien
5	261	12.7	831	PRLR_CHICK	Q04594 gallus gall
6	241	11.7	415	I15R_MOUSE	P21183 mus musculus
7	238	11.6	831	PRLR_MELGA	Q91094 meleagris g
8	220	10.7	369	PRLR_HUMAN	P31785 mus sapien
9	216.5	10.5	830	PRLR_COLL	Q90374 columba liv
10	212.5	10.3	369	CVRG_MOUSE	P34902 mus musculus
11	208	10.1	373	CVRG_CANFA	P40321 canis famil
12	195	9.5	878	I13B_MOUSE	P28954 mus musculus
13	189.5	9.2	379	CVRG_BOVIN	Q95118 bos taurus
14	178.5	8.7	897	CVRG_HUMAN	P32927 homo sapien
15	173.5	8.4	896	CVRG_MOUSE	P26955 mus musculus
16	165	8.0	581	PRLR_BOVIN	Q28172 bos taurus
17	165	8.0	610	PRLR_RAT	P05710 rattus norv
18	159	7.7	608	PRLR_MOUSE	Q08501 mus musculus
19	151	7.3	622	PRLR_HUMAN	P16471 homo sapien
20	151	7.3	862	I12S_HUMAN	Q99665 homo sapien
21	150.5	7.3	917	I16B_MOUSE	Q00560 mus musculus
22	150	7.3	581	PRLR_CEREL	Q28235 cervus elap
23	149	7.2	616	PRLR_RABIT	P14787 oryctolagus
24	142.5	6.9	400	GMCR_HUMAN	P15509 homo sapien
25	138	6.7	378	I13R_HUMAN	P26951 homo sapien
26	134.5	6.5	1097	PRLR_HUMAN	P42702 homo sapien
27	131.5	6.4	630	PRLR_ORENT	Q91513 oreochromis
28	128	6.2	874	I12S_MOUSE	P97378 mus musculus
29	126.5	6.2	918	I16B_HUMAN	P40189 homo sapien
30	120.5	5.9	836	GMCR_HUMAN	Q99062 homo sapien
31	113.5	5.5	1165	I13R_MOUSE	P48357 homo sapien
32	112.5	5.5	1630	PTP1_DROME	P35992 drosophila
33	109.5	5.3	918	I16B_RAT	P40190 rattus norv

RESULT 1

ID	I132_HUMAN	STANDARD;	PRT;	380 AA.
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13 BINDING PROTEIN).			
GN	IL13RA2 OR IL13R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Renal cell carcinoma;			
RX	MEDLINE=96279273; PubMed=8663118;			
RA	Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N., Ferrara P.;			
RA	"Cloning and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha chain.;"			
RT	J. Biol. Chem. 271:16921-16926(1996).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RA	Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H., Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;			
RA	Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=973221053; PubMed=9177784;			
RA	Guo J., Aplou F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;			
RA	"Chromosome mapping and expression of the human interleukin-13 receptor.;"			
RT	Genomics 42:141-145(1997).			
CC	- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13 (IL-13), BUT NOT TO IL-4.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.			
CC	- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; X95302; CAA64617.1; -			
DR	EMBL; U70981; AAB17170.1; -			
DR	EMBL; Y08768; CAA70021.1; -			
DR	MIM; 300130; -			

34	107.5	5.2	638	1	GHR_HUMAN	P10912 homo sapien
35	107.5	5.2	837	1	GCSR_MOUSE	P40223 mus musculus
36	107	5.2	634	1	GHR_BOVIN	P79108 bos taurus
37	106	5.2	634	1	GHR_SHEEP	Q28575 ovis aries
38	105	5.1	511	1	VGLG_VSVO	P04884 vesicular s
39	104.5	5.1	1092	1	LIFR_MOUSE	P19756 sus scrofa
40	102.5	5.0	638	1	GHR_PIG	P19941 oryctolagus
41	101.5	4.9	638	1	GHR_RABIT	Q62959 rattus norv
42	99.5	4.8	1162	1	LEPR_RAT	P16310 rattus norv
43	99	4.8	638	1	GHR_RAT	P48356 mus musculus
44	98.5	4.8	1162	1	LEPR_MOUSE	P04883 vesicular s
45	98	4.8	511	1	VGLG_VSVIG	

ALIGNMENTS

DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT DISULFID 184 197
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 360CBIB5562C887 CRC64;

Query Match 100.0%; Score 2056; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 7.3e-161;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYFLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPPLSLD 60
Db 1 MAFVCLAIGCLYFLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPPLSLD 60

QY 61 HFKECTVEVELKYRNGISGTWTITITKNLHYKDGFDLNGIEAKIHTLLPWQCTNGSEVQ 120
Db 61 HFKECTVEVELKYRNGISGTWTITITKNLHYKDGFDLNGIEAKIHTLLPWQCTNGSEVQ 120

QY 121 SSWAETTYWISQGPETKVDQMDCVYVNWQYLLCSWKPGLVLDNTNLYFWYEGLDH 180
Db 121 SSWAETTYWISQGPETKVDQMDCVYVNWQYLLCSWKPGLVLDNTNLYFWYEGLDH 180

QY 181 ALQCVDYIKADGONIGCRPPYLEASDYKDFYICVNGSSNKPFRSSYFFQONIVKPLP 240
Db 181 ALQCVDYIKADGONIGCRPPYLEASDYKDFYICVNGSSNKPFRSSYFFQONIVKPLP 240

QY 241 PVLNFTRESSCEIKLWSIPGLGPAPCFDYEIREDDTLTVATVENETYLTKTNE 300
Db 241 PVLNFTRESSCEIKLWSIPGLGPAPCFDYEIREDDTLTVATVENETYLTKTNE 300

QY 301 TRLQCFVRSKNVNYCSDGISEWSDKQWEGEDLSKTLRLFWLPFGFILLVIFVTG 360
Db 301 TRLQCFVRSKNVNYCSDGISEWSDKQWEGEDLSKTLRLFWLPFGFILLVIFVTG 360

QY 361 LLRLRPNTYPKM 372
Db 361 LLRLRPNTYPKM 372

RESULT 2
IL5R_HUMAN STANDARD; PRT; 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125 ANTIGEN).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuppens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;
RT "Molecular basis of the membrane-anchored and two soluble isoforms of
the human interleukin 5 receptor alpha subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
[3]
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=92005669; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuppens T., van der Heyden J.,
RA Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of
an IL5-specific alpha chain and a beta chain shared with the receptor
for GM-CSF";
RL Cell 66:1175-1184(1991).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/co/cdw125.htm".

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

DR EMBL; M96652; AAA59152.1; -
DR EMBL; M96651; AAA59151.1; -
DR EMBL; M75914; AAA36110.1; -
DR EMBL; A26249; CAA01793.1; -
DR EMBL; A24587; CAA01731.1; -
DR EMBL; A26251; CAA01794.1; -
DR PIR; A40267; A40267.
DR MIM; 147851; -
DR InterPro; IPR000950; -
DR InterPro; IPR002465; -
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420
FT DOMAIN 21 342
FT TRANSMEM 343 362
FT DOMAIN 363 420
FT CARBOHYD 35 35
FT CARBOHYD 131 131
FT CARBOHYD 216 216
FT CARBOHYD 244 244
FT VARSPPLIC 333 335
FT VARSPPLIC 336 420
FT VARSPPLIC 333 333
FT VARSPPLIC 334 420
SQ SEQUENCE 420 AA; 47700 MW; 420681FBC6B51700 CRC64;
INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
NDE -> FSR (IN SOLUBLE ISOFORM S1).
MISSING (IN SOLUBLE ISOFORM S1).
N -> K (IN SOLUBLE ISOFORM S2).
MISSING (IN SOLUBLE ISOFORM S2).
MISSING (IN SOLUBLE ISOFORM S2).
420681FBC6B51700 CRC64;

Query Match 15.1%; Score 309.5; DB 1; Length 420;
Best Local Similarity 27.6%; Pred. No. 4.4e-18;
Matches 98; Conservative 65; Mismatches 151; Indels 41; Gaps 15;

QY 27 DTEIKVNPQDFEIVDPGVLGYLQWQPPPLSLDFKCEVTELYKYRNGISGTWTITIT 86
Db 25 DEKISLPPVNFITIKVTG-LAQVLLQWPNPDQEQ-RNVNLEYQVKINAPKEDDIETIT 82

RC TISSUE-B-cell;
RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
RA Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
RA Eugster H.P., Bonnefoy J.Y.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-T-cell;
RX MEDLINE=97067184; PubMed=8910586;
RA Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S.,
RA Leonard W.J.;
RT "cDNA cloning and characterization of the human interleukin 13
RT receptor alpha chain.";
RL J. Biol. Chem. 271:29265-29270(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.
CC -!- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER,
CC SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
CC KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y10659; CAA71669.1; -
DR EMBL; Y09328; CAA70508.1; -
DR EMBL; U62858; AAB37127.1; -
DR EMBL; U81379; AAD00510.3; -
DR HSP; P31785; 1ILN.
DR MIM; 300119; -
DR Interpro: IPR001777; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 21
FT CHAIN 22 427
FT DOMAIN 22 343
FT TRANSMEM 344 367
FT DOMAIN 368 427
FT DOMAIN 39 102
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CONFLICT 130 130
FT CONFLICT 358 358
FT SEQUENCE 427 AA; 48759 MW; 5983B3E8F554107B CRC64;

Query Match 14.3%; Score 294.5; DB 1; Length 427;
Best Local Similarity 26.3%; Pred. No. 7.5e-17;
Matches 101; Conservative 59; Mismatches 161; Indels 63; Gaps 18;
QY 11 LYTELITSTFTGCTSSDTEIKVNPDPDFIVDPGLVLYLQWQPPPLSLDHFKECTVEY- 69
DB 10 LWALLCAGGGGGGGAAPTEPPVNLNLSVENLCTVITWNPPEGAS--SNCLWTF 67
QY 70 -----ELKYRNIGSETWKTITLKNLHYKDFLUNKIEAKIHTLLPWQC-TNGSEVOSSWA 124
DB 68 SHFGDKQDKKIAPETRRSI-----EVLNERICLQVGS---QCSNTESEKPSILV 114
QY 125 ETTYWIS-POGIPETKQVDMCVYVNWQYLLCSWPGICVLDTNLYNFYTWEGDLHALQ 183
DB 115 EKC--ISPPEGDPESAVALTELOCIWNLNLSYMKCSWLPGRNTSPDTNLYYHRSLEKTHQ 172
QY 184 CVDYIKADQNGICRFPYLEASD--YKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLPP 241
DB 173 C-ENIFREGQYGCDFDLTKVDSSEFQHSVQIMVKNAGKIKPSENVPLTSRVKPPDP 231
QY 242 --VYITFTRESSCEIKLKWISPLGPICPACFDYIEIREDDT-----LYTATVENETY 293
DB 232 HIKNLSFND---DLVQWENPQNEI-SRCLFYEVVNNSTQETHNVFYVQEAKEPDEF 287
QY 294 TLKTTNETRQLCFVY-----RSKNVIYC-SDDGIWSEWSDKQCEGEDLSKK 339
DB 288 ERNVENTS---CFMVGVLVPLDTNVRIRVTKNLCYEDDDKLWNNWSEDM-----SIGKK 339
QY 340 TLLRFLWPLFGFLLIVFVFTGLLL 363
DB 340 RNSTLYIT--MLLIVPVIVAGAIL 361
RESULT 5
PRLR_CHICK STANDARD; PRT; 831 AA.
AC Q04594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPRLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE-Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
RT the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL; D13154; BAA02439.1; -
DR PIR; JQ1655; JQ1655.

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DR HSP: P16471; lbp3.
DR InterPro: IPR000950; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002465; -.
DR Pfam: PF00041; fn3; 4.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADB95 CRC64;

Query Match 12.7%; Score 261; DB 1; Length 831;
Best Local Similarity 26.3%; Pred. No. 9.2e-14;
Matches 98; Conservative 55; Mismatches 175; Indels 44; Gaps 16;

QY 18 TFGCTSSDTEIKVN--PPQDFE---IVDPG-----YLGYLILQWOPPLSL 59
Db 97 TTFNITVATNEIGNSDPOQVDVTSIVQSPVNLFLTKRSANIMYLWAKWSPPLLA 156

QY 60 DHFKECTVEYELKYNIGSETWKTITKNLHKDGLNKGIEAKIHTLLPWOCTNGSEV 119
Db 157 DASSNHYELRIKPEKEWETI---SVGVQTOCKINR-LNAGRRYVQVRCITLDGE 212

QY 120 QSSWAEYTWISPGQ-IPETKVQDMCVYNNQYLLCSWKPGIGVLLDTNYNLFYWEGL 178
Db 213 WSEWSSERHILIPSQSPPEKPTIICRSPKETFTCWKPGLDGHPNTVTLYSKEGE 272

QY 179 DHALOCVDYKADGONICRPPYLEADYKDFYICVNGSSSENKPIRSSYFFQLQNIKVP 238
Db 273 EQVYECPDY-RTAGPN-SCYFDKHTSEWTYINITVATNEMGNSSDPHYVDYTIYQP 330

QY 239 LPPVYLTFTRESSCEIK---LKWS-IPLGPIPARCFDYEIFEIR---EDDTLVTATVEN 290
Db 331 DPPVNVTLLEKPKINRKYVLVLTWSPPLADVRSGWLITLEYELRLKPEGEWEWEIFVQ 390

QY 291 ET-YTLKTTNETROLQCFVVRKVNLYCSDD--GINSWSDKQCWE-GBDLSKKTLLRFLW 346
Db 391 QTOYKMFSLNPKKKYI-----IQHCKPDHGHGSWSENSENYIQIPNDFRVKDMI-VMI 443

QY 347 PFGFTLILVIFV 358
Db 444 VLGVLSSLICLI 455

RESULT 6
IL5R_MOUSE
ID IL5R_MOUSE STANDARD; PRT; 415 AA.
AC P21183;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA).
GN IL5RA OR IL5R.
OS Mus musculus (Mouse).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092260; PubMed=2265612;
RA Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RA Takatsu K.;
RT "Molecular cloning and expression of the murine interleukin-5
receptor";
RL EMBO J. 9:4367-4374(1990).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
CC ON B-CELLS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -----
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CC -----
DR EMBL: D90205; BAA14231.1; -.
DR PIR: S12357; S12357.
DR MGI: MGI:96558; IL5ra.
DR InterPro: IPR000950; -.
DR InterPro: IPR002465; -.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 415
FT DOMAIN 18 339
FT TRANSMEM 340 361
FT DOMAIN 362 415
FT DISULFID 131 152
FT DISULFID 179 191
FT CARBOHYD 32 32
FT CARBOHYD 128 128
FT CARBOHYD 213 213
FT CARBOHYD 241 241
SQ SEQUENCE 415 AA; 46989 MW; A4326D2922571C08 CRC64;

Query Match 11.7%; Score 241; DB 1; Length 415;
Best Local Similarity 24.9%; Pred. No. 1.7e-12;
Matches 88; Conservative 65; Mismatches 144; Indels 56; Gaps 17;

QY 34 PPQDFEIVDPGYLYLQWQPLSLDHFKECTVEYELKYNIGSETWKTITKNLHKYD 93
Db 29 PPNVTIKATG-LAQVLLHWDPNPQEQ-RHVDLEVHKINAPQEDYDTRKTES---KC 83

QY 94 GFDLNGKIEAKIHTLLPWOCTNGSEVQSSWAEYTWISPGIGVLLDTNYNLFYWEGLDHALQCVDIK-ADGONICRPP- 149
Db 84 VTPLEHGFASVRTILK---SSHTTTLASSWSAEL-KAPPGSPGTSVTNLCTTHTVSS 139

QY 150 -----WQY-LILCSWKPGIGVLLDTNYNLFYWEGLDHALQCVDIK-ADGONICRPP- 200
Db 140 HTHLRPYQVSLRCTLWLVGKDAPEDQYFLYRFGVLTE--KQEYSRDLALNRNTACWFR 197

QY 201 -YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLQNIKVPPLPVLTFTRESSCEIKLWS 259
Db 198 TFINSKGFQELAVHINGSKRAAIKPPQDLFSPLADQVNPNNVTVEESN-SLYIQWE 256

QY 260 IPLGPIPARCFDYEIFEIRDD-----TTLVATVENETVTLKTTNETROLQCFV 308
Db 257 KPLSAFPDHCNFYELKIYNTKNGHIQKEKLIANKFISKIDDVSTYSIQ-----V 305
```


RA Willard H., Henthorn P.S.;
 RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated
 in X-linked severe combined immunodeficiency, SCID1X1";
 RA Hum. Mol. Genet. 2:1099-1104(1993).
 RL [4]
 RN
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE-94090315; PubMed-8266076;
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
 RA Arai K.-I., Sugamura K.;
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
 RT receptors for IL-2 and IL-4";
 RL Science 262:1874-1877(1993).
 RN [5]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE-94090317; PubMed-8266078;
 RA Russell S.M., Kkegan A.D., Harada N., Nakamura Y., Noguuchi M.,
 RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-4 receptor";
 RL Science 262:1880-1883(1993).
 RN [6]
 RP IDENTIFICATION AS A IL-7R SUBUNIT.
 RX MEDLINE-94090316; PubMed-8266077;
 RA Noguuchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-7 receptor";
 RL Science 262:1877-1880(1993).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE-95111955; PubMed-829123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling";
 RL Structure 2:839-851(1994).
 RN [8]
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE-94130970; PubMed-8299698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 RA de Saint Basile G.;
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 RT severe combined immunodeficiency disease result in the loss of
 RT high-affinity IL-2 receptor binding";
 RL Eur. J. Immunol. 24:475-479(1994).
 RN [9]
 RP VARIANT XSCID LYS-68.
 RX MEDLINE-94375038; PubMed-8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 RT the interleukin-2 receptor gamma chain gene in SCID1X1 that
 RT differently affect the mRNA processing";
 RL Genomics 21:291-293(1994).
 RN [10]
 RP VARIANT XSCID HIS-162.
 RX MEDLINE-94300093; PubMed-8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 RT receptor gamma-chains in patients with X-linked severe combined
 RT immunodeficiency";
 RL J. Immunol. 153:1310-1317(1994).
 RN [11]
 RP VARIANT XSCID ASN-39.
 RX MEDLINE-95023932; PubMed-7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 RT chromosome-linked severe combined immunodeficiency with peripheral T
 RT cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
 RN [12]

RP VARIANTS XSCID CYS-226 AND HIS-226.
 RX MEDLINE-95397841; PubMed-7668284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 RT gene causing human X-linked severe combined immunodeficiency";
 RL Am. J. Hum. Genet. 57:564-571(1995).
 RN [13]
 RP VARIANT XSCID SER-183.
 RX MEDLINE-96013903; PubMed-7557965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 RA Levinsky R.L., Kinnon C.;
 RT "Screening for mutations causing X-linked severe combined
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand
 RT conformation polymorphism analysis";
 RL Hum. Genet. 96:427-432(1995).
 RN [14]
 RP VARIANT XSCID GLN-237 G-H-W INS.
 RX MEDLINE-95164726; PubMed-7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 RT gamma-chain mutation causing X-linked severe combined
 RT immunodeficiency";
 RL J. Clin. Invest. 95:895-899(1995).
 RN [15]
 RP VARIANT XSCID GLN-271.
 RX MEDLINE-95190013; PubMed-7883965;
 RA Schmalstieg F.C., Leonard W.J., Noguuchi M., Berg M., Rudloff H.E.,
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 RT moderate form of X-linked combined immunodeficiency";
 RL J. Clin. Invest. 95:1169-1173(1995).
 RN [16]
 RP VARIANT XSCID ARG-115.
 RX MEDLINE-97042245; PubMed-8900089;
 RA Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B., Fischer A.,
 RA Mueller-Fleckenstein I., Horneff G., Schroten H.,
 RA de Saint Basile G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 RT spontaneous reversion of the genetic defect in T cells";
 RL New Engl. J. Med. 335:1563-1567(1996).
 RN [17]
 RP VARIANT XSCID GLN-285.
 RX MEDLINE-97295088; PubMed-9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 RA Cant A., Kinnon C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 RT common gamma chain mutation";
 RL Hum. Genet. 99:677-680(1997).
 RN [18]
 RP VARIANT XSCID CYS-222.
 RX MEDLINE-98064061; PubMed-9399950;
 RA Sharfe N., Shahar M., Roifman C.M.;
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 RT morphology";
 RL J. Clin. Invest. 100:3036-3043(1997).
 CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 INTERLEUKINS.
 CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
 IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMGLOBULINEMIA, SWISS TYPE
 OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide C0132 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd132.htm".
 CC -!- DATABASE: NAME=IL2RGbase; NOTE=X-linked SCID mutation database;
 CC WWW="http://www.nhgri.nih.gov/DIR/GMBS/SCID/".
 CC -----
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CC -----
 CC EMBL; D11086; BAA01857.1; -
 CC EMBL; L12183; AAA59145.1; -
 CC EMBL; L12178; AAA59145.1; JOINED.
 CC EMBL; L12176; AAA59145.1; JOINED.
 CC EMBL; L12177; AAA59145.1; JOINED.
 CC EMBL; L12179; AAA59145.1; JOINED.
 CC EMBL; L12180; AAA59145.1; JOINED.
 CC EMBL; L12181; AAA59145.1; JOINED.
 CC EMBL; L12182; AAA59145.1; JOINED.
 CC EMBL; L19546; AAC37524.1; -
 CC PIR; A42565; A42565.
 CC PDB; 1ILM; 26-JAN-95.
 CC PDB; 1ILN; 26-JAN-95.
 CC MIM; 308380; -
 CC MIM; 300400; -
 CC InterPro; IPR000950; -
 CC InterPro; IPR00177; -
 CC InterPro; IPR002465; -

Query Match 10.7%; Score 220; DB 1; Length 369;
 Best Local Similarity 25.5%; Pred. No. 7.7e-11;
 Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

QY 97 LNKGIKATHTLTPWCTNGSE-VQSSWAETTYWISPOQIPETKVDMDCVYNNQYLIC 155
 DB 19 LGVGLNTLT-----PNGNEDTADFFLTMTDLSVSTLPLPEVQCFFVFNVMNC 72
 QY 156 SW-----KPGIGVLLDNYNLFYVYEGLDH--ALQVDYIKADGNICRFPYLEASDY 207
 DB 73 TWNSSEPPQ-----TNLTHYTKNSDNDKVKCKSHYLFSEITSCGQLOKKEIHL 125
 QY 208 KDFYICVNGSSSENKPIRSYFTFQIQNIYKPLPPVYLTFTRESSCBKIKWSIPLGPIPA 267
 DB 126 QTFVVLQDPRE--PRQATQMLKQLNVLIPAPENLTLHLKLSQLELNWN---NRFNL 180
 QY 268 RCFDYIEIREO-DITLVATVE-NETYLYKTNETROLCFVVRKYNVICSDDGIWSEW 325
 DB 181 HCLEHLVQYRTDWDHSWTQSDYRHKFSLPSVDGQKRYTFVRFRNPLCGSAQHWSEW 240
 QY 326 SDKQCEGEDLSKLTLLRFLWPGFLLILVIFWTG 360
 DB 241 SHPIHW-GNSTKEN-----PFLFAEAVVISVG 268

RESULT 9
 ID PRLR COLLI STANDARD; PRT; 830 AA.
 AC Q90374.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
 GN PRLR.
 OS Columba livia (Domestic pigeon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
 OX NCBI_TaxID=8932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cropsac;
 RX MEDLINE=94283267; PubMed=7516866;
 RA Chen X., Horseman N.D.;
 RT "Cloning, expression, and mutational analysis of the pigeon prolactin
 RT receptor."
 RL Endocrinology 135:269-276(1994).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC -!- PROLACTIN.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC EMBL; U07694; AAA20646.1; -
 CC HSSP; P16471; 1BP3.
 CC InterPro; IPR000950; -
 CC InterPro; IPR00177; -
 CC InterPro; IPR002465; -
 CC Pfam; PF00041; fn3; 4.
 CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 830
 FT DOMAIN 24 439
 FT TRANSMEM 440 460
 FT DOMAIN 461 830
 FT DOMAIN 25 122
 FT DOMAIN 123 226
 FT DOMAIN 229 326
 FT DOMAIN 327 429
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304
 FT CARBOHYD 316 316
 FT CARBOHYD 336 336
 FT SEQUENCE 830 AA; 94507 MW; 3B074E83CDF69EFF CRC64;

Query Match 10.5%; Score 216.5; DB 1; Length 830;
 Best Local Similarity 24.4%; Pred. No. 4e-10;
 Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;
 QY 18 TTFGCTSSSDTEIKVNPQDFEIVDPGYLG-----DPQYVDVTSIVQDAPVNLSELTSTASTYLLAKW 150
 DB 97 TTYNTVWAMNEIGSNSS-----DPQYVDVTSIVQDAPVNLSELTSTASTYLLAKW 150
 QY 54 QPPLSLDHFKECTV-EYELKYRNISETWKTITITKNLHYKDFGLNKGIEAKIHTLLPWQ 112
 DB 151 SPPLADVTNSHVRYELRLAKEKEWETV---SVGVQTOYKYNR-LQAGVKYVVQVR 206
 QY 113 CTNGSEVSSWAETTYWISPOG-IPETKYQDMDCVYNNQYLCSWKPGIGVLLDTNLYL 171
 DB 207 CVLDIGENSEWSSERRHIHPNGESPPEKPTIIKRSPEKETFTCWKPGSDGHPNTYTL 266
 QY 172 FWYEGDLHALOCVDYIKADGNICRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQ 231
 DB 267 LYSKEGEERYEPCDY-KTAGPN-SCYFDKKTSTFWTYNTITVTKATNEIGSNVSDPLYVD 324
 QY 232 LQNIKPLPPVYLTFTRESSCEIK-----LKWS-IPLGPIPA--RCFDYIEIREDDTTLV 284
 DB 325 VTYIVQTDPPVNVTLLEKKTVNRKYLVTWSPPLADVRSGLWTLIDYELRLKPEA--- 381
 QY 285 TATVENETYTLTNETROLCFVW---RSKYNVICSDD--GIWSEWS-DKQCWEGEDLS 337
 DB 382 -----EEMETIFVQQTTHYKMFSLNPGKKYIVQIHKPDHGSWSEWSLEKYLQIPTDFR 436
 QY 338 KKTLLRFLWPGFILLIVIFV 358
 DB 437 IKDMV-VMIIVGVLSLCLV 456

RESULT 10
CYRG_MOUSE
ID CYRG_MOUSE STANDARD; PRT; 369 AA.
AC P34502;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277575; PubMed=8503926;
RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT "Cloning of the mouse interleukin 2 receptor gamma chain:
RT demonstration of functional differences between the mouse and human
RT receptors.";
RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBA/CA;
RX MEDLINE=93391374; PubMed=8378320;
RA Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
RT IL-2R gamma chain expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93366191; PubMed=8359699;
RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RT gamma.";
RL Gene 130:303-304(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104285; PubMed=7805729;
RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
RA Fischer A., de Saint Basile G.;
RT "The murine interleukin-2 receptor gamma chain gene: organization,
RT chromosomal localization and expression in the adult thymus.";
RL Eur. J. Immunol. 24:3014-3018(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S;
RX MEDLINE=96341745; PubMed=8750189;
RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
RA Dougherty G.J.;
RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT the adhesion protein CD44.";
RL J. Neuroconcol. 26:231-239(1995).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; D13821; BAA02974.1; -
DR EMBL; U21795; AAA64279.1; -
DR EMBL; D13565; BAA02760.1; -
DR EMBL; L20048; AAA39286.1; -
DR EMBL; S75852; AAB32904.1; -
DR EMBL; S75844; AAB32904.1; JOINED.
DR EMBL; S75845; AAB32904.1; JOINED.
DR EMBL; S75847; AAB32904.1; JOINED.
DR EMBL; S75848; AAB32904.1; JOINED.
DR EMBL; S75849; AAB32904.1; JOINED.
DR EMBL; S75850; AAB32904.1; JOINED.
DR EMBL; S75851; AAB32904.1; JOINED.
DR EMBL; S75851; AAB32904.1; JOINED.
DR EMBL; S75851; AAB32904.1; JOINED.
DR PIR; JN0592; JN0592.
DR PIR; JN0775; JN0775.
DR MGD; MGI:96551; IL2rg.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 369
FT DOMAIN 23 263
FT TRANSMEM 264 284
FT DOMAIN 285 369
FT DOMAIN 151 250
FT DISULFID 62 72
FT DISULFID 102 115
FT CARBOHYD 71 71
FT CARBOHYD 75 75
FT CARBOHYD 84 84
FT CARBOHYD 96 96
FT CARBOHYD 159 159
FT CARBOHYD 164 164
SQ SEQUENCE 369 AA; 42241 MW; CB2D5AB459077AC7 CRC64;
Query Match 10.3%; Score 212.5; DB 1; Length 369;
Best Local Similarity 26.9%; Pred. No. 3.1e-10;
Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;
QY 136 PETKQDMDVYNNQYLKCSN---KPGIGVLDTNLYNLYWYEGLDHAL--QCVDYIK 189
DB 53 PFLPLVEVCFVFNEIYMNCSTWNSSEPQA-----TNLTHRYKVSNDNFTQECSHYLF 107
QY 190 ADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNIVKPLPPVYLTFTRE 249
DB 108 SKEITSGCOIQKEDIQYTFVVL--QDPQKQRAVQKLNQNLVIRAPENLTLSNL 165
QY 250 SGEIKLKWISIPGIPARCFYEIRED-DTTLVATVENE-TYTLKTTNETROLCFV 307
DB 166 SESQLELRWK--SRHIERCLQYLVQYRNSDRSMTLIVNHEPRSLPSVDLKRKYTER 223
QY 308 VRSKYNICSDGIGSEWSKOCWEG----EDLSKTLIRFWLPFGF--ILLIVIVTGL 361
DB 224 VRSYRNPIGSSQSKWSQPVHNGSHTVENPFLFAELVLPVGTMLITLIFVYCW 283
QY 362 LLRKENTYP 370
DB 284 LERMPPIPP 292
RESULT 11
CYRG_CANFA
ID CYRG_CANFA STANDARD; PRT; 373 AA.
AC P40321;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)

Query Match 9.5%; Score 195; DB 1; Length 878;
Best Local Similarity 24.1%; Pred. No. 2.4e-08;
Matches 86; Conservative 59; Mismatches 150; Indels 62; Gaps 23;

QY 34 PPQDEIVDPGYLYLOWQPPPL---SLDHKECTVEYELAKYRIGSTWTKITKLNH 90
DB 139 PKPDHISPSG---DHFLLEWSLGDQSQVSWLSKDIEFEVAYKRL-QDSWED--ASSLH 193
QY 91 YKDGFDLNGKIEAKTHTLPL-----WQCTNGSEQV---SSWAETTYWISPOGIPET 138
DB 194 -TSNQVN--LEPKL--FLPNSIYARVTRLSAGSSLSGRPSRWSPVHWSQPG-DKA 247
QY 139 KYODMDCVYNNQYLICSWKPGIGVLLDTNLYNLFYEGDLHALQCVDIKADGONI--- 195
DB 248 QPONLQCFDGIOSLHCSWVWTTQTSVSGFLFYRPSAPAEKCSPPVVKPEQASVYTR 307
QY 196 -CRRPYLEADYKDFYICVNGSSSENKPIRSSYFTFQONIVKPLPPVY-LFTTRESCE 253
DB 308 YRCSLPVPPEPSAHSQYTSVRHLEQKFT-MSYHIQME-----PPILNQTKNRDS--- 357
QY 254 IKLKSIPGLPIPARCFD--YEIETREDTTLVATVEN---EYTLKTTNETRQLCFV 307
DB 358 YSLHETOKIP---KIIDHTFQVQKKSESWKDSTENLGRVNSMDLPQLEPDPYSYCAR 414
QY 308 VRSK-VNIYCSDDGIWSEMSDKQWEGEDLSKKTLLRFLWLPFGFILLIIVFTGLLL 363
DB 415 VRVKPISDY---DGIWSEMSNEYTW-TDWMPTL---WI-----VLIIVFLIFTLL 460

RESULT 13
CYRG_BOVIN
ID CYRG_BOVIN STANDARD; PRT; 379 AA.
AC Q95118;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96268473; PubMed=8672241;
RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
gamma gene."
RL DNA Cell Biol. 15:453-459(1996).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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or send an email to license@isb-sib.ch).

DB EMBL; U33748; AAB07812.1; -.
DB HSSP; P31785; 1ILN.
DB InterPro; IPR000950; -.
DB InterPro; IPR001777; -.
DB InterPro; IPR002465; -.

DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 290 POTENTIAL.
FT DOMAIN 291 379 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 158 256 FIBRONECTIN TYPE-III.
FT DISULFID 68 78 POTENTIAL.
FT DISULFID 109 122 POTENTIAL.
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 9.2%; Score 189.5; DB 1; Length 379;
Best Local Similarity 26.2%; Pred. No. 2.5e-08;
Matches 62; Conservative 42; Mismatches 106; Indels 27; Gaps 9;

QY 135 IPETKQDMDCVYNNQYLLCSW-----KPGIGVLLDTNLYNLFYWY---EGLDHALQCV 185
DB 61 LPLPKVQ---CFVFNVEYMNCTWNSSEPP-----NNLTLYGYRNFNGDKLQECG 110
QY 186 DYKADGQNICRFPYLEADYKDFYICVNGSSSENKPIRSSYFTFQONIVKPLPPVILT 245
DB 111 HYLSEGITSGCWGKKEIRLYETVFWQDPRHR--KQPKOMLKLQDLQVLPWAPENIT 168
QY 246 FTRESCEIKLKSIPGLPIPARCFDYEIETRED--DTTLVATVEN--EYTLKTTNETRQ 303
DB 169 LNLSEFQLELWS---NRYLDCHLEHLVQYRSDRDSRWTEQSDVDRHSFSLPSVDAQKL 225
QY 304 LCFVVRKVNVIYCSDDGIWSEMSDKQWEGEDLSKKTLLRFLWLPFGFILLIIVFTVG 360
DB 226 YTFVRVRSRYNPLCGSAQHSWDSYPIHW-GSNTSKENIENPENPSLFALEAVLPIG 281

RESULT 14
CYRG_HUMAN
ID CYRG_HUMAN STANDARD; PRT; 897 AA.
AC P32927;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR (CDW131 ANTIGEN).
GN CSF2RB OR IL5RB OR IL3RB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91088571; PubMed=1702217;
RA Hayashida K., Kitamura T., Gorman D.M., Arai K., Yokota T.,
RA Miyajima A.;
RT "Molecular cloning of a second subunit of the receptor for human
granulocyte-macrophage colony-stimulating factor (GM-CSF):
reconstitution of a high-affinity GM-CSF receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
RN [2]
RP REVISION TO 454.
RA Kitamura T.;
RL Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

```
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw131 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw131.htm".  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL: M59941; AAA18171.1; -  
CC PIR: A39255; A39255.  
CC MIM: 138981; -  
CC InterPro: IPR000950; -  
CC InterPro: IPR001777; -  
CC InterPro: IPR002465; -  
CC Pfam: PF00041; fn3; 2.  
CC PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.  
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 16  
FT CHAIN 17 897 CYTOKINE RECEPTOR COMMON BETA CHAIN.  
FT DOMAIN 17 443 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 444 460 POTENTIAL.  
FT DOMAIN 461 897 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 129 238 FIBONECTIN TYPE-III.  
FT DOMAIN 336 434 FIBONECTIN TYPE-III.  
FT DISULFID 35 45 BY SIMILARITY.  
FT DISULFID 75 91 BY SIMILARITY.  
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 346 346 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 897 AA; 97335 MW; 3398E37FDB8F393A CRC64;  
  
Query Match 8.7%; Score 178.5; DB 1; Length 897;  
Best Local Similarity 22.5%; Pred. No. 5.6e-07;  
Matches 89; Conservative 57; Mismatches 144; Indels 105; Gaps 21;  
  
QY 32 VNPQDFEIVDPGYLG- - - - -LYLQWQPP- - - - -LSLDHF- - - - - 62  
DB 97 VPCSFVVDVDFSPQDRPLGLRLVTLLQHVQPPEDRLQISTDODHLLTWSVAL 156  
  
QY 63 - - - - -KECTVEYELKYNIGSETW- - - - -TIITKNLHYKDGFDLKNKIE- - - - -A 103  
DB 157 GSPQSHWLSPGDLEFVYVKRL-QDSWEDAAILLNTS- - - - -QATLGPHEHLMPSSTYVA 210  
  
QY 104 KIHT-LLPQCTNGSEVQSSWAETTYWISPGIPETKVDMDCVYNNQYLLCSWKPGIG 162  
DB 211 RVTRTLAGPSRLSGR--PSKWSPEVCWDSQPG-DEAQPNLECFDFDGAAVLSCSWEVRKE 267  
  
QY 163 VLLDNTNLYFWYEGLDHALQCVDIKADGONIG- - - - -CRFPYLEASDYKDFYICVN 215  
DB 268 VASSVFGFLYKPSDAGEECPVLR- - - - -EGLSLHTRHHQCIQVPPQATHGQIVSVQ 324  
  
QY 216 GSSENKPIRSSYFTFQLQINVLPLPPVLTFTRESSCEIKLKWISPLGPPIPARCFDYEIE 275  
DB 325 PRRAEKHIVSV- - - - -NI--QMAPPSLNVTKGD-SYSLRWETMKRYEHIHDTFEIQ 375  
  
QY 276 IREDDTLVTAT-VENEYTLKTN- - - - -ETRLQCFV-VRSKNYICSDPDGIVSE 324  
DB 376 YRKD- - - - -TATWKDSKTEITLQNAHSMALPALEPSTRYKWARVRVTRTSRTY- - - - -NGIWS 427  
  
QY 325 WSDKOCWEGEDLSKTLRLLPFGFILLIVFT 359  
DB 428 WSEARSWTESV- - - - -LPMWVLIVIFLT 453  
  
RESULT 15  
ID CYRB_MOUSE STANDARD; PRT; 896 AA.  
AC P26955;  
DT 01-OCT-1993 (Rel. 27, Created)
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DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR.  
GN CSF2RB OR CSF2B1 OR AIC2B OR IL3RB1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90319131; PubMed=1695379;  
RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,  
RA Yahara I., Arai K., Miyajima A.;  
RT "Cloning and expression of a gene encoding an interleukin 3 receptor-  
RT like protein: identification of another member of the cytokine  
RT receptor gene family".  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).  
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5  
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.  
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA  
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -!- SIMILARITY: CONTAINS 2 FIBONECTIN TYPE III-LIKE DOMAINS.  
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL: M34397; AAA37204.1; -  
CC PIR: A35782; A35782.  
CC MGD: MGI:1339759; Csf2rb1.  
CC InterPro: IPR000950; -  
CC InterPro: IPR001777; -  
CC InterPro: IPR002465; -  
CC Pfam: PF00041; fn3; 2.  
CC PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.  
CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 896 CYTOKINE RECEPTOR COMMON BETA CHAIN.  
FT DOMAIN 23 441 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 442 463 POTENTIAL.  
FT DOMAIN 464 896 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 132 241 FIBONECTIN TYPE-III.  
FT DOMAIN 343 440 FIBONECTIN TYPE-III.  
FT DISULFID 39 49 BY SIMILARITY.  
FT DISULFID 77 94 BY SIMILARITY.  
FT CARBOHYD 62 62 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 896 AA; 99111 MW; 8CE16EDFDC07A999 CRC64;  
  
Query Match 8.4%; Score 173.5; DB 1; Length 896;  
Best Local Similarity 20.7%; Pred. No. 1.4e-06;  
Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;  
  
QY 5 CIAIGCLTFLITSTFGCTS- - - - -SSDTEIK- - - - -VNPPQDFEIVDPGYLG 48  
DB 94 CVPRCVPY- - - - -IRFSITNEDYISFRPDSDLGIQLMPLAQNVQPLPKNVISSEDR 150  
  
QY 49 LYLQWQPP- - - - -SLDHFKECTVEYELKYNIGSETWTKITKN- - - - -LHYKDGFDLKNK 100  
DB 151 FLENSVSLGDAQVSWLSSKDIIEFVAYKRL-QDSWEDAYSLSHTSKFQVNFEPKLFLENS 209  
  
QY 101 IEA-KIHT-LLPQCTNGSEVQSSWAETTYWISPGIPETKVDMDCVYNNQYLLCSWK 158  
DB 210 IYAPRVTRTLAGPSRLSGR--PSRWSPEAHWDSQPG-DKAPQPNLQCFDFDGIQSLHCSWE 266
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:03 ; Search time 60.7 Seconds
(without alignments)
371.534 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_372
Perfect score: 2056
Sequence: 1 MAPVCAIGCLYFLISTTF.....ILVIFVTGLLRKPNTPYK 372

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0601.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2056	100.0	380	AAW24972	Human interleukin-
2	2056	100.0	380	AAW35295	Human IL-13 bindin
3	2056	100.0	380	AAW36613	Human Zcytor2 cyto
4	2056	100.0	380	AAW41520	Human HR-1 recepto
5	2056	100.0	380	AAW41502	Human cytokine/pep
6	2056	100.0	380	AAW33603	Homo sapiens HR-1
7	2056	100.0	380	AAW35296	IL-13 binding chai
8	2056	100.0	380	AAW72136	Human interleukin
9	2056	100.0	380	AAW29748	Human IL-13 recept
10	2030	98.7	380	AAW36614	Human Zcytor2 cyto
11	1853	90.1	372	AAW36616	Celebus macaque Zc

ALIGNMENTS

RESULT 1
AAW24972
ID AAW24972 standard; protein; 380 AA.
AC AAW24972;
DT 22-JUN-1998 (first entry)
XX Human interleukin-13 beta receptor.
DE Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
KW Homo sapiens.
XX OS
XX PN W03720926-A1.
XX PD 12-JUN-1997.
XX PF 07-NOV-1996; 96WO-FR01756.
XX PR 06-DEC-1995; 95FR-0014424.
XX PA (SNFI) SANOFI SA.
XX PI Caput D, Ferrara P, Laurent P, Vita N;
XX DR WPI; 1997-319773/29.
XX DR N-PSDB; AAT85826, AAT86464.
XX PT New purified human interleukin-13 receptors - and related nucleic
XX acids, useful for diagnosis and treatment of inflammation, allergy,
XX etc
XX Claim 1; Figure 2a; 83pp; French.

Mature interleukin
Construct containi
Murine IL-13 bindi
IL-13 binding chai
Murine interleukin
Mouse IL-13 recept
Interleukin-13 bin
Sequence of human
Sequence of secret
Human interleukin-
Human IL-5 recepto
Sequence of human
Protein used in pr
Human interleukin-
Human interleukin-
Human interleukin-
Mouse interleukin-
IL5-R-GFP 130 fusi
Soluble human IL-5
shIL-5R-alpha. Sy
Human interleukin-
IL-13/IL-4 dual tr
IL-13/IL-4 dual tr
Sequence of interl
Sequence of interl
Sequence of interl
Sequence of interl
Sequence of interl
IL-2 receptor gamm
IL-2 receptor gamm
Murine IL-2R gamma
Human cytokine rec

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are designated IL-13R beta and alpha respectively.
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R beta
 CC and alpha which can be used as IL-13 antagonists, specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for gene
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunoassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFLISTTFCGTSSTDEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
 DB 1 mafvclaigclytlflisttfgctssdteikvnpqdfelvdpvglylylqwpplslid 60

QY 61 HFKECTVEYELKYRNISETWKTITIKNLHYKDGFDLKNKGTEAKHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkyrnisetwktititknhykdgfdlnkgleakhtllpwqctngsevg 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWOYLKCSWKPGLVLDNTNLYFYWEGLDH 180
 DB 121 sswaettywispgipetkvqdmcdvynnwoyllkcswkpglgvldntnlyfywegldh 180

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQLQNIKPLP 240
 DB 181 alqcvdyikadqngicrcfpyleasdykdfyicvngssenkprrsytfqlqniakplp 240

QY 241 PVLFTRESSECEIKLWSIPGPAPRCFDEYIEIREDDTLVTATVENETYLKTTNE 300
 DB 241 pvlftressceiklwsipgiparcfdeyieireddtlvtatvenetylkttnne 300

QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKOCWEGEDLSKTKTLRFLWLPFGFILLVIFVTG 360
 DB 301 trqlcfvvrksvniycsddgiwsewsdkocwegedlsktktlrlfllwlpfgflllvifvtg 360

QY 361 LLLLRKNTYPKM 372
 DB 361 llllrkntypkm 372

RESULT 2

AAW35295
 ID AAW35295 standard; Protein: 380 AA.

XX
 AC AAW35295;

XX
 DT 27-MAR-1998 (first entry)

XX
 DE Human IL-13 binding chain of the IL-13 receptor.

XX
 KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.

XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= signal_sequence
 FT /note= "putative"
 FT Protein 26..380
 FT /label= mature_protein
 FT Domain 26..341
 FT /label= extracellular_domain
 FT Domain 342..362
 FT /label= transmembrane_domain
 FT Domain 363..380
 FT /label= intracellular_domain

XX WO9731946-A1.

PD 04-SEP-1997.

XX 28-FEB-1997; 97WO-US03124.

XX 01-MAR-1996; 96US-0609572.

XX (GEMY) GENETICS INST INC.

XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;

XX WPI; 1997-448632/41.

DR N-PSDB; AAT95214.

XX New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transformed cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis

XX Claim 11; Pages 34-35; 49pp; English.

XX The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied,
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.

XX Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFLISTTFCGTSSTDEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60

DB 1 mafvclaigclytlflisttfgctssdteikvnpqdfelvdpvglylylqwpplslid 60

QY 61 HFKECTVEYELKYRNISETWKTITIKNLHYKDGFDLKNKGTEAKHTLLPWQCTNGSEVQ 120

DB 61 hfkectveyelkyrnisetwktititknhykdgfdlnkgleakhtllpwqctngsevg 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWOYLKCSWKPGLVLDNTNLYFYWEGLDH 180

DB 121 sswaettywispgipetkvqdmcdvynnwoyllkcswkpglgvldntnlyfywegldh 180

QY 181 ALQCVDIKADQNGICRPPYLEASDYKDFYICVNGSSNKPIRSSYTFQIQNIVKPLP 240
Db 181 alqcvdyikadqngicrpfyleasdykdfyicvngssnkpirssytfqlqnvkplp 240
QY 241 PVLFTRESSCEIKLWSIPLGPPIPARCFDYEIEIREDDTLVTATVENETYLKTTNE 300
Db 241 pvlftressceiklwsiplgppiparcfdyeieireddtlvtatvenetytkttne 300
QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGEDLSKTLRLFWLPGFILLVIFVTG 360
Db 301 trqlcfvvrsvniycsddgiwsewsdkcwegedlsktlrlfwlpgfllilvifvtg 360
QY 361 LLRKPNTPYPM 372
Db 361 llrrkpnptypm 372

RESULT 3
AAW36613
ID AAW36613 standard; Protein; 380 AA.
XX AC AAW36613;
XX AC
DT 30-MAR-1998 (first-entry)
XX DE Human zcytor2 cytokine receptor protein.
XX KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Domain 340..363
FT /label= transmembrane_domain
FT Domain 364..380
FT /label= intracellular_domain
FT Domain 25..339
FT /label= ligand_binding_domain
XX PN WO9733913-A1.
XX PD 18-SEP-1997.
XX PF 12-MAR-1997; 97WO-US04043.
XX PR 13-MAR-1996; 96US-0013345.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
PI O'Hara PJ;
XX WPI; 1997-470820/43.
XX DR N-PSDB; AAT96782.
XX PT New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
XX PS Claim 2; Page 47-48; 79pp; English.
XX CC This sequence represents a novel ligand-binding receptor, zcytor2,
CC which shares homology with cytokine receptors and was isolated from human
CC placental polyA+ RNA. The resulting polypeptide is a receptor for
CC cytokines (particularly interleukin-13) and is expressed on the surface
CC of testicular cells, probably being involved in spermatogenesis. It can
CC be used to detect ligands that promote proliferation and/or
CC differentiation of such cells in cultures and may also be used to treat
CC infertility. Antagonists of this receptor may be used to characterise
CC ligand-receptor interactions and as male-specific contraceptives. By
CC blocking the action of IL-13, receptor antagonists and ligand-binding
CC this receptor can also be used to modulate immune function, e.g. in

CC allergy and asthma, as a diagnostic to determine circulating levels of
CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.
XX SQ Sequence 380 AA;
Query Match 100.0%; Score 2056; DB 18; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.5e-192;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTFLLISTTGTCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWOPPLSLD 60
Db 1 mafvclaigcltyflisttgtctssdteikvnpqdfeidvpgylglylylqwpplsl 60
QY 61 HFKECTVEYELKYRNIGSETWKTITKLNHYKDGFDLKNKIEAKIHTLLPWOCTNGSEVQ 120
Db 61 hfkectveyelkyrnigsetwktitklnhykdgfdlnkgleakihltlpwqctngse 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSWKPGLVLLDTNLYNLFYWYEGLDH 180
Db 121 sswaettywispgipetkvqdmcdvyyvwnqyylcswkpgigvlltdnynlfywyegldh 180
QY 181 ALQCVDIKADQNGICRPPYLEASDYKDFYICVNGSSNKPIRSSYTFQIQNIVKPLP 240
Db 181 alqcvdyikadqngicrpfyleasdykdfyicvngssnkpirssytfqlqnvkplp 240
QY 241 PVLFTRESSCEIKLWSIPLGPPIPARCFDYEIEIREDDTLVTATVENETYLKTTNE 300
Db 241 pvlftressceiklwsiplgppiparcfdyeieireddtlvtatvenetytkttne 300
QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGEDLSKTLRLFWLPGFILLVIFVTG 360
Db 301 trqlcfvvrsvniycsddgiwsewsdkcwegedlsktlrlfwlpgfllilvifvtg 360
QY 361 LLRKPNTPYPM 372
Db 361 llrrkpnptypm 372

RESULT 4
AAW41520
ID AAW41520 standard; Protein; 380 AA.
XX AC AAW41520;
XX AC
DT 22-JUN-1998 (first entry)
XX DE Human HR-1 receptor.
XX KW HR-1 receptor; human; cytokine; infection; asthma; allergy;
KW haematopoietic disorder; tumour; therapy; diagnosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Sig_peptide
FT Protein 22..380
FT /label= Mat_protein
XX PN WO9747741-A1.
XX PD 18-DEC-1997.
XX PF 12-JUN-1996; 96WO-US10262.
XX PR 12-JUN-1996; 96WO-US10262.
XX PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
PI Appelbaum ER, Hu J;
XX
DR WPI: 1998-052308/05.
DR N-PSDB; AAV04131.
XX
XX Nucleic acid sequence encoding human cytokine peptide hormone
PT receptor - useful to treat, prevent or diagnose, e.g. lowered
PT resistance to infection, asthma, allergy or haematopoietic disease
XX
PS Claim 13; Page 62-64; 76pp; English.
XX
CC This protein comprises a novel human cytokine/peptide hormone
CC receptor, designated the HR-1 receptor, that shows 27% identity
CC and 52% similarity to the interleukin-5 receptor. Its amino acid
CC sequence was deduced from a cDNA clone (see AAV04131) obtained from
CC human testis library. Recombinant HR-1 receptor can be expressed
CC in claimed host cells, and used in a claimed method for identifying
CC compounds which bind to, and activate or inhibit, it. HR-1
CC receptor activators and agonists can be used to treat, prevent or
CC diagnose predisposition to lowered resistance to infection, asthma,
CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer.
CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
CC be used to treat conditions associated with HR-1 receptor
CC overexpression. The antibodies can also be used to determine HR-1
CC receptor levels, since overexpression may be diagnostic of tumours.
XX
XX Sequence 380 AA: SQ

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Query Match      100.0%; Score 2056; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.5e-192;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dd	1	mafvciaigclytflistftgctsssdteikvnppqdfelvdpgylylqlwqpplslid	60
Qy	61	HFEKCTVEYELKYRNIGSEFWKTIIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEQV	120
Dd	61	hflectveyelkrynigsetwtiiitknhykdgfdlnkgieakihlllpwqctngseqv	120
Qy	121	SSWAETTYWISPGGIPETKVQDMDCVYYNNQYLCLCSWKPGIGVLDTNYNLFWYBGLDH	180
Dd	121	sswaettywispggipetkvgdmdevyywnwqylcswkpgigvldtnynlfwyegldh	180
Qy	181	ALQCVDYIKADGONICGRPYLEASDYKDFYICVNGSSENKKPRSSSYFFQLOINVKPILP	240
Dd	181	alqcvdyyikadgnigcrfpyleasydkdfycvngssenkprrsyfftfqiqlnvkplp	240
Qy	241	PVYLTTRESSCEIKLWSIPLGPIDPARCFDYIEIREDDTTLVTATVENETVTLKTNE	300
Dd	241	pvytlftressceiklwsiplgpiparcfdyieireddttlvtatvenetytlktne	300
Qy	301	TROLCFVRSKVNIYCSDDGINSWDKQCBEGEDLSKKTLLRFWLPPFGILLIYLVFVTG	360
Dd	301	trqlcfvrskvniycsdgdginswdkqcbegedissktllrflwpfgfillilvifvtg	360
Qy	361	LLLLRKPNPTYPKM 372	
Dd	361	lllrkpnptypkm 372	
RESULT	5		
AAW41502			
ID	AAW41502	standard; Protein; 380 AA.	
XX	XX		
XX	AAW41502;		
XX	XX		
XX	08-JUN-1998	(first entry)	
DE	Human cytokine/peptide receptor, HR-1 receptor.		

XX	HR-1 receptor; cytokine receptor; peptide hormone receptor; human;	
KW	infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;	
KW	neutropenia; therapy.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
Peptide	1..21	
FT	/label= Sig_peptide	
FT	22..380	
FT	/label= Mat_protein	
FT	/note= "Claim 14"	
XX		
PN	EP812913-A2.	
XX		
PD	17-DEC-1997.	
XX		
PF	04-JUN-1997; 97EP-0303815.	
XX		
PR	12-JUN-1996; 96US-0017843.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(SMIK) SMITHKLINE BEECHAM CORP.	
XX		
PI	Appelbaum ER, Hu J;	
XX		
DR	WPI; 1998-034974/04.	
DR	N-PSDB; AAV04075.	
XX		
PT	Human cytokine/peptide hormone receptor, HR-1 receptor - useful to	
PT	increase resistance to infections in individuals with trauma and/or	
PT	burns	
XX		
PS	Claim 13; Page 27-28; 34pp; English.	
XX		
CC	This protein comprises a novel human cytokine/peptide hormone	
CC	receptor, designated HR-1 receptor. The amino acid sequence	
CC	was deduced from a cDNA clone (see AAV04075) isolated from a human	
CC	testis cDNA library. It shows 27% amino acid identity and 52%	
CC	similarity with the human interleukin-5 receptor. Also claimed are	
CC	polynucleotides encoding HR-1 receptor, vector and host cells, an	
CC	antagonist to the polypeptide, antibody against the polypeptide, an	
CC	antagonist that inhibits the activity of the polypeptide, a process	
CC	for diagnosing a disease, or a susceptibility to disease, related	
CC	to expression of HR-1 receptor, and a method for identifying	
CC	compounds that activate or inhibit the HR-1 receptor. HR-1	
CC	receptor protein and polynucleotides can be used for research,	
CC	biological, diagnosis and (gene) therapy applications, e.g. to	
CC	increase resistance to infections in individuals with trauma and/or	
CC	burns, and to prevent, ameliorate, treat, diagnose and/or determine	
CC	predisposition to asthma, allergic disorders or disorders of	
CC	hematopoiesis induced by AIDS, aplastic anaemia, congenital or	
CC	cyclic neutropenia or as a consequence of cytotoxic therapy of	
CC	cancer, lymphoma, leukaemia and/or bone marrow transplantation.	
XX		
SQ	Sequence 380 AA;	

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Query Match      100.0%; Score 2056; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.5e-192;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	MAFVCLAIGCLYTLFISTTGCCTSSSDTEIKVNPDPDEFIVDPGYLYLQWQPPSLSD	60
Db	1	mafvciaigcllytlfsttgcctsssdteikvnpdpdefivdpgylylylwqppslsd	60
QY	61	HFEKCTVEYELKRYNIGSETWKTIIIRKNLHYKDGDFDLNKIEAKIHTLLPWQCTNGSEVQ	120
Db	61	hfekctveyelkrynigsetwktliiknlhykdgfdlnkgieakihtllpwqctngsevg	120
QY	121	SSWAETTYWTSPOGIPETKVDMDCVVYNQYLLCSWKPGIGVLLDTNYNLPFYWEGLOH	180

Db 121 sswaettywispqgipetkvqmdcvynwqyllcswkpgigvllidtnynlfywyegldh 180
QY 181 ALQCVDYIKADGQNTGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNVKPLP 240
Db 181 alqcvdyikadgqngicrfpyleasdykdfyicvngssenkprrssyftfqiqlnvkplp 240
QY 241 PVLFTRESSCEIKLWSIPLGPIPARCFDYEIREDDDTLVATVENETYLTKTNE 300
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QY 301 TRQLCFVVRKSNVYCSDDGIWSEWSKQCEGDELKTLRFLWLPFGFILLVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewsdkqcegedlskllrflwlpfgfllilvifvtg 360
QY 361 LLRLRPNTYPKM 372
Db 361 llrlrkpntypkm 372
RESULT 6
AAW33603
ID AAW33603 standard; Protein; 380 AA.
XX
AC AAW33603;
DT 08-JUN-1998 (first entry)
XX
DE Homo sapiens HR-1 receptor.
XX
KW Cytokine; hormone receptor; AIDS; acquired immune deficiency;
KW syndrome; aplastic anaemia; neutropenia; cancer treatment;
KW infection resistance; diagnosis; tumours; HR-1 receptor;
KW asthma; allergic; haematopoietic; disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
XX
PN WO9747742-A1.
XX
PD 18-DEC-1997.
XX
PF 09-JUL-1996; 96WO-US11459.
XX
PR 12-JUN-1996; 96WO-US10262.
PR 12-JUN-1996; 96US-0017843.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMK) SMITHKLINE BEECHAM CORP.
XX
PI Appelbaum ER, Hu J;
XX
DR WPI; 1998-052309/05.
DR N-PSDB; AAV02295.
XX
PT DNA encoding human cytokine-peptide hormone receptor - useful for
PT treating preventing or diagnosing, e.g. lowered resistance to
PT infection, asthma, allergy, or haematopoietic disease
XX
PS Claim 15; Fig 1; 75pp; English.
XX
CC The sequence is that of the human cytokine/peptide hormone receptor
CC (HR-1 receptor). This, or its activators or agonists, can be used to
CC treat, prevent or diagnose predisposition to lowered resistance to
CC infection, asthma, allergic or haematopoietic disorders, e.g. where
CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
CC neutropenia or cytotoxic treatments for cancer. Antagonists of the
CC receptor, e.g. antibodies or fragments of it may be used to treat
CC conditions associated with overexpression of the HR-1 receptor, e.g.
CC those listed above. Antibodies may also be used to assay levels of HR-1
CC receptor, overexpression of which may be diagnostic of tumours, by usual

CC immunoassays; to isolate and identify HR-1 receptor-expressing cells; or
CC for affinity purification of the HR-1 receptor.
SQ Sequence 380 AA;
Query Match 100.0%; Score 2056; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.5e-192;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYFTLIISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
Db 1 mafvclaigclyftliistftgctssdteikvnpqdfeidvpgylglylqwpplslid 60
QY 61 HPEKCTVEYELKYNIGSETWKTILTKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
Db 61 hpektveyelkynigsetwktiltnlhykdgfdlnkgleakihltpwqctngsevq 120
QY 121 SSWAETTYWISPGIPETKVQMDCVYVNWQYLLCSWKPGLVLLDTNLYNFYWEGLDH 180
Db 121 sswaettywispqgipetkvqmdcvynwqyllcswkpgigvllidtnynlfywyegldh 180
QY 181 ALQCVDYIKADGQNTGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNVKPLP 240
Db 181 alqcvdyikadgqngicrfpyleasdykdfyicvngssenkprrssyftfqiqlnvkplp 240
QY 241 PVLFTRESSCEIKLWSIPLGPIPARCFDYEIREDDDTLVATVENETYLTKTNE 300
Db 241 pvlftressceiklwsiplgpiiparcfdyeyeireddttlvtatvenetytlktne 300
QY 301 TRQLCFVVRKSNVYCSDDGIWSEWSKQCEGDELKTLRFLWLPFGFILLVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewsdkqcegedlskllrflwlpfgfllilvifvtg 360
QY 361 LLRLRPNTYPKM 372
Db 361 llrlrkpntypkm 372
RESULT 7
AAW33603
ID AAW33603 standard; Protein; 380 AA.
XX
AC AAW33603;
DT 12-SEP-2000 (first entry)
XX
DE IL-13 binding chain of human IL-13 receptor.
XX
KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; antiallergic;
KW antiinflammatory; antiasthmatic; vaccine.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /note= "signal peptide"
FT Protein 26..380
FT /note= "mature protein"
FT Domain 26..341
FT /note= "extracellular domain; a polypeptide
FT comprising amino acids 22-334 is
FT specifically claimed in Claim 11(e)"
FT 342..362
FT /note= "transmembrane domain"
FT Domain 363..380
FT /note= "intracellular domain; a polypeptide
FT comprising amino acids 257-383 is
FT specifically claimed in Claim 11(f)"
XX

PN WO200036103-A1.
XX 22-JUN-2000.
PD 13-DEC-1999; 99WO-US29493.
PF 14-DEC-1998; 98US-0211335.
XX (GEMY) GENETICS INST INC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
PI Wills-Karp M;
XX WPI; 2000-431587/37.
DR N-PSDB; AAA27912.
XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
PT an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
PT asthma, Grave's disease and inflammatory conditions of the lung -
XX Claim 11(d); Page 53-54; 60pp; English.
XX The present sequence is that of the interleukin-13 binding chain
CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated
CC human testis cDNA clone (see AAA27912). IL-13bc is a member of
CC the haematopoietin receptor family that acts as a mediator of
CC IL-13. The invention provides methods for the recombinant
CC production of IL-13bc polypeptides, including claimed full-length
CC IL-13bc, its extracellular domain, and its intracellular domain.
CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
CC of IL-13 and its receptor) can be used to treat conditions in
CC which IL-13 is implicated, particularly IgE-mediated conditions and
CC diseases including atopy, allergy, asthma, immune complex diseases
CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
CC thyroiditis and Grave's disease), lung inflammation,
CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
CC activation, IL-13bc proteins can also be used to enhance macrophage
CC activation, e.g. in vaccination, treatment of mycobacterial or
CC intracellular organisms or parasite infections. IL-13bc proteins
CC may also be used to potentiate the effects of IL-13 in vitro and
CC in vivo, as diagnostic agents, and to screen for agents capable of
CC binding to IL-13bc or IL-13 receptor, or which interfere with the
CC binding of IL-13 to its receptor.
XX
SQ Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 21; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.5e-192;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLATGCLTYFLISTFGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPLSLD 60
Db 1 mafvclatgcltyflistfgctssdteikvnpqdfeidvdpgylylqwgplslid 60
QY 61 HFKECTVEYELKYRIGSETWKTITITNLHYKDGFDLANKGEAKHTLLPWQCTNGSEVQ 120
Db 61 hfkectveyelkyrnigsetwktititnlhykdgfdlnkgeakhtllpwqctngsevq 120
QY 121 SSWAETTYWISPGQIPETKVQDMDCVYVNWQYLLCSWRKPGIGVLDDTNVLFYWYEGLDH 180
Db 121 sswaettywispgqipetkvqdmdevynwqyllcswkpgigvllldtnvlnfywyegldh 180
QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYTFQLONVKPLP 240
Db 181 alqcvdyikadqngicrfpyleasdykdfyicvngssenkiprissytfqlqnvkplp 240
QY 241 PVIYLTRESSCEIKLWSIPGLPTPARCFDYETREIRDDTTLVTATVENETYLKTTNE 300
Db 241 pviyftressceiklwsiplgiparfcfdyeyreirddtltvtatvenetylktktne 300

QY 301 TRQLCFVVRKSVNIYCSDDGIWSEWSDKQCEGDLSSKTLRLFWLPEGFILILVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewdskqcegedlskktllrflwlpfgfillilvifvtg 360
QY 361 LLRLKPNTPYPM 372
Db 361 llrlkpnptypkm 372
RESULT 8
AAAY72136
ID AAY72136 standard; Protein; 380 AA.
XX
AC AAY72136;
XX
DT 24-APR-2001 (first entry)
XX Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
DE Human; IL-13; interleukin-13 binding chain of IL-13 receptor; IL13bc;
XX therapy; tissue fibrosis; Schistosoma infection; surgical incision;
KW cytostatic; wound; IL-13 related condition; allergic condition;
KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;
KW macrophage activation.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Peptide 1..25 /label= Signal_peptide
FT Region 1..81 /note= "This region is identical to the translated
FT sequence of an expressed sequence tag (EST) identified
FT as y999f10.rl human cDNA clone 41648 5"
FT Protein 26..380 /label= Mature_human_interleukin (IL)-13_binding_chain-
FT of_IL-13_receptor
FT Domain 26..341 /note= "Extracellular domain; this region is specifically
FT claimed in claims 1e, 6e, 15e and 23e"
FT Domain 342..362 /note= "Transmembrane domain"
FT Domain 363..380 /note= "Intracellular domain; this region is specifically
FT claimed in claims 1f, 6f, 15f and 23f"
XX
PN WO200078336-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-US17103.
XX
PR 21-JUN-1999; 99US-0334512.
XX (GEMY) GENETICS INST INC.
PA (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
PI Wills-Karp M;
XX WPI; 2001-080753/09.
DR N-PSDB; AAD02335.
XX Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
PT in a mammalian subject, involves administering a pharmaceutical
PT composition comprising IL-13 antagonist -
XX Claim 1a; Page 69-70; 72pp; English.
XX The invention relates to a method of treating, or inhibiting
CC the formation of tissue fibrosis in mammals, which involves
CC administering a pharmaceutical composition comprising interleukin
CC (IL)-13 antagonist. The protein of the invention is useful for

CC treating tissue fibrosis resulting from infection with Schistosoma
 CC or from healing of a wound which is a surgical incision, or
 CC inhibiting formation of tissue fibrosis which affects tissues such
 CC as liver, skin epidermis and endodermis, muscle, tendon, cartilage,
 CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
 CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,
 CC biliary tract and gut. It is also used in the treatment or modulation
 CC of various IL-13 related conditions such as allergic conditions,
 CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.
 CC The present sequence is human interleukin (IL)-13
 CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used
 CC to potentiate the effects of IL-13. This protein is also used to
 CC enhance macrophage activation and hence can be used in vaccination
 CC or treatment of mycobacterial or parasitic infections.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIGCLYTLSTFTGCTSSDTEIKVNPQDPFEIVDPGVLGYLYLQWQPPSLD 60
 Db 1 mafvclaigcltytlstftgctssdteikvnpqdpfeivdpvglylylqwqpplsl 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITTKNLHYKDGFDLNKGTEAKHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkyrnigsetwktitknlhykdgfdlnkgeakhtllpwqctngsevg 120
 QY 121 SSWAETTYWISPGQIPETKVDMDCVYNNWOYLCSWKPGLGVLLDTNYNLFYWEGLDH 180
 Db 121 sswaettywispgqipetkvdmdcvynnwqylcswkpglgvlltdntnynlfywegldh 180
 QY 181 ALQCVDIYKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQLOINVKPLP 240
 Db 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkprrssyftfqlqnvkplp 240
 QY 241 PVYLTFRESSCEIKLWSIPLGPAPCFDYEIRDDDTLTATVENETYLTKTNE 300
 Db 241 pvytlftressceiklwsiplgpiarcfdyeiredddtltatvenetylktktne 300
 QY 301 TRQLCFVVRKSVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
 Db 301 trqlcfvvrsvknlycsddgiwsewskqwedlskktllrflwlpfgfillilvifvtg 360
 QY 361 LLLRKPNTYPRM 372
 Db 361 lllrkpntyprkm 372

RESULT 9
 AAB29748
 ID AAB29748 standard; Protein; 380 AA.
 XX
 AC AAB29748;
 XX
 XX
 XX
 DT 23-FEB-2001 (first entry)
 XX
 DE Human IL-13 receptor IL-13 binding chain (IL-13bc).
 XX
 KW Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
 KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnerary;
 KW wound healing; schistosoma infection; liver; skin; muscle;
 KW cartilage; cardiac tissue; lung tissue; uterine tissue;
 KW intestinal tissue; vascular tissue; neural tissue.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO200064944-A1.
 XX
 PD 02-NOV-2000.
 XX

PF 28-APR-2000; 2000WO-US11612.
 XX
 PR 28-APR-1999; 99US-0301808.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 XX Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;
 PI Whitters MJ, Wood C;
 XX
 XX WPI; 2001-024676/03.
 DR N-PSDB; AAC81416.
 XX
 XX Treating or inhibiting tissue fibrosis resulting from infection with
 PT schistosoma and wound healing involves administering interleukin-13 or
 PT interleukin-4 antagonist
 XX
 XX Claim 1; Page 76-77; 82pp; English.
 XX
 XX The invention relates to a method of treating fibrosis in a mammal
 CC by administering an interleukin-13 (IL-13) antagonist or an IL-4
 CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding
 CC chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or
 CC soluble fragments thereof. The method is useful for treating or
 CC inhibiting the formation of tissue fibrosis resulting from the healing
 CC of a wound, including a surgical incision wound, or from infection with
 CC schistosoma. The method may be used to treat fibrosis in a variety of
 CC tissues, particularly liver tissue, but also skin epidermis, skin
 CC endodermis, muscle, tendon, cartilage, cardiac tissue, pancreatic
 CC tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,
 CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut
 CC tissue. The present sequence represents human IL-13bc.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2056; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.5e-192;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIGCLYTLSTFTGCTSSDTEIKVNPQDPFEIVDPGVLGYLYLQWQPPSLD 60
 Db 1 mafvclaigcltytlstftgctssdteikvnpqdpfeivdpvglylylqwqpplsl 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITTKNLHYKDGFDLNKGTEAKHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkyrnigsetwktitknlhykdgfdlnkgeakhtllpwqctngsevg 120
 QY 121 SSWAETTYWISPGQIPETKVDMDCVYNNWOYLCSWKPGLGVLLDTNYNLFYWEGLDH 180
 Db 121 sswaettywispgqipetkvdmdcvynnwqylcswkpglgvlltdntnynlfywegldh 180
 QY 181 ALQCVDIYKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQLOINVKPLP 240
 Db 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkprrssyftfqlqnvkplp 240
 QY 241 PVYLTFRESSCEIKLWSIPLGPAPCFDYEIRDDDTLTATVENETYLTKTNE 300
 Db 241 pvytlftressceiklwsiplgpiarcfdyeiredddtltatvenetylktktne 300
 QY 301 TRQLCFVVRKSVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
 Db 301 trqlcfvvrsvknlycsddgiwsewskqwedlskktllrflwlpfgfillilvifvtg 360
 QY 361 LLLRKPNTYPRM 372
 Db 361 lllrkpntyprkm 372

RESULT 10
 AAW36614
 ID AAW36614 standard; Protein; 380 AA.
 XX
 AC AAW36614;

Query Match 90.1%; Score 1853; DB 18; Length 372;
Best Local Similarity 92.2%; Pred. No. 1.6e-172;
Matches 343; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAFVCLATGCLYTLISTFGCTSSDSEIKVNPQDFEIVDPGGYLYLQWQPPLSLD 60
DB 1 mafvylalrcictflistftgyststdeikvnpqdfiwdpgylylqwgppslid 60

QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLANKTEAKHTLLPWQCTNGSEVQ 120
DB 61 nfkectveyelkynigsetwtitknlhykdgfdlnkgleakhtllpwqctngsevg 120

QY 121 SSWAETTWISQGIPEKVKQDMCVYNNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH 180
DB 121 sswaeatywispqgipetkvgmdcvyynwqyllcswkpgigvlldtynlnfywyegldr 180

QY 181 ALOCVDYIKADGONIGCRFPYLEADSYKDFYICVNGSSENKPIRSSYTFQNLQNVKPLP 240
DB 181 alqcvdyikvqgnlgrcfpylessdkdfyicvngsssetkpirssytfqlqnvkplp 240

QY 241 PVLFTRESSCEIKLWSIPLGPIPARCFDYEIREDDTTLVTATVENETYLTKTNE 300
DB 241 pvlftctgeslyeiklwsiplgpiarpcfyeieireddttltvtatvenetytlktne 300

QY 301 TRQLCFVVRKVNIIYCSDDGIWSEWSKQCEGEDLSKTLRLRFLPFGFILLIFVFTG 360
DB 301 trqlcfvvrskvniiycsddgiwsewsdkqceveellkktlllflpfgfllilvifvtg 360

QY 361 LLLRPNTPYPM 372
DB 361 lllckrdsypkm 372

RESULT 12
AAW56261
ID AAW56261 standard; Protein; 315 AA.
XX AC AAW56261;
XX DT 16-SEP-1998 (first entry)
XX DE Mature interleukin-13 binding protein.
XX KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
XX KW autoimmune disease; antibody; immunotherapy.
XX OS Homo sapiens.
XX PN W09810638-A1.
XX PD 19-MAR-1998.
XX PF 10-SEP-1997; 97WO-AU00591.
XX PR 27-FEB-1997; 97AU-0005374.
XX PR 10-SEP-1996; 96AU-0002262.
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX DR WPI; 1998-207062/18.
XX DR N-PSDB; AAV22702.
XX PT New isolated interleukin-13 binding protein - used to develop
XX PT products for therapy e.g. for allergic conditions such as asthma or
XX PT for diagnosis or detection
XX PS Disclosure; Page 55-56; 69pp; English.
XX CC The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for

treating IL-13 mediated conditions such as certain allergic conditions
such as asthma or to inactivate locally administered IL-13 after IL-13
treatment. The products can also be used as diagnostic agents, e.g. for
detecting autoimmune diseases. The antibodies can also be used for
immunotherapy and may also be used as a diagnostic tool.

SQ Sequence 315 AA;

Query Match 85.3%; Score 1753; DB 19; Length 315;
Best Local Similarity 100.0%; Pred. No. 7.1e-163; Mismatches 0; Gaps 0;
Matches 315; Conservative 0;

QY 29 EIKVNPQDFEIVDPGGYLYLQWQPPLSLDHFKECTVEYELKYNIGSETWKTITKN 88
DB 1 eikvnpqdfiwdpgylylqwgppslidhfkectveyelkynigsetwktitkn 60

QY 89 LHYKDGFDLANKTEAKHTLLPWQCTNGSEVSSWAETTWISQGIPEKVKQDMCVY 148
DB 61 lhykdgfdlnkgleakhtllpwqctngsevgsswaettywispqgipetkvgmdcvy 120

QY 149 NWOYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALOCVDYIKADGONIGCRFPYLEASDYK 208
DB 121 nwqyllcswkpgigvlldtynlnfywyegldhalqcvdyikadgngicrpfyleasdyk 180

QY 209 DFYICVNGSSENKPIRSSYTFQNLQNVKPLPVPVLTFTRESSCEIKLWSIPLGPIPAR 268
DB 181 dfyicvngssenkpirssytfqlqnvkplppvyltftressceiklwsiplgpiar 240

QY 269 CPDYEIREDDTTLVTATVENETYLTKTNETROLCFVVRKVNIIYCSDDGIWSEWSK 328
DB 241 cfdyeieireddttltvtatvenetytlkktnetrqlcfvvrskvniiycsddgiwsewsdk 300

QY 329 QCWEGEDLSKTLRL 343
DB 301 qcwegedlskttlrl 315

RESULT 13
AAW56260
ID AAW56260 standard; Protein; 359 AA.
XX AC AAW56260;
XX DT 16-SEP-1998 (first entry)
XX DE Construct containing mature interleukin-13 binding protein.
XX KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
XX KW autoimmune disease; antibody; immunotherapy.
XX OS Homo sapiens.
XX PN W09810638-A1.
XX PD 19-MAR-1998.
XX PF 10-SEP-1997; 97WO-AU00591.
XX PR 27-FEB-1997; 97AU-0005374.
XX PR 10-SEP-1996; 96AU-0002262.
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX DR WPI; 1998-207062/18.
XX DR N-PSDB; AAV22701.
XX PT New isolated interleukin-13 binding protein - used to develop
XX PT products for therapy e.g. for allergic conditions such as asthma or
XX PT for diagnosis or detection

Example 14; Page 52-53; 69pp; English.

The IL-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one IL-13 activity. They can be used for treating IL-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered IL-13 after IL-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.

AA	Sequence	359 AA;
SQ		

Query Match	85.3%	Score 1753;	DB 19;	Length 359;
Best Local Similarity	100.0%;	Pred. No. 8.6e-163;		
Matches 315; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	29	EIKVNPQDEIVDPGYLYLQWQPLSLDHDFKECTVEYELKRYNIGSSTWKTITKN	88	
Db	45	eikvnpqdeivdpgylylqwpplsldhfkectveyelkrynigsetwktilcnn	104	
QY	89	LHYKDGFDLANKGIEBAKIHTLLPMQCTNGSEVQSSWAETTYWISPGQIPETKQVDMDCVY	148	
Db	105	lhykdgfdlankgteakihntllpqwctngsevqsswaettywispgqipetkvqdmdcvyy	164	
QY	149	NWOYLLCSWKPGGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNTIGCRFPYLEASDYK	208	
Db	165	nwoyllcswkpgigvllldtnynlfiwyegldhalqcvdyikadgqngicrfpyleasdyk	224	
QY	209	DFYICVNGSSENKPIRSSYTFQLOINVKPLPPVYLLFTRESSCEIKLWSIPIGPPIPAR	268	
Db	225	dfyicvngssenkprrssytfqilqnvkplppvylftressceiklwsipigprip	284	
QY	269	CFDYEIEIRBDDTLVATVENENYTIKTTNETROLCFVVRSKYNIYVSCDDGIWSEMSDK	328	
Db	285	cfdyeiieirddtlvtatvenetytktttnetrlqcfvvrskynlycsddgiwsemsdk	344	
QY	329	QCWEGEDLSKKTLLR	343	
Db	345	qcwqedliskktllr	359	

RESULT 14
AAW35294
ID AAW35294 standard; Protein: 383 AA.

AA
AC AAW35294;

27-MAR-1998 (first entry)

DE Murine IL-13 binding chain of the IL-13 receptor.

Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
allergy; asthma; immune complex disorder.

AA
OS

Key	Location/Qualifiers
Peptide	1..21
FT	/label= signal_sequence
FT	/note= "putative"
FT	22..383
Protein	/label= mature_protein
FT	22..334
Domain	/label= extracellular_domain
FT	335..356
Domain	/label= transmembrane_domain
FT	357..383
Domain	/label= intracellular_domain
FT	

PN WO9731946-A1.

XX

04-SEP-1997.

AA 28-FEB-1997: 97WO-US03124.

AA 01-MAR-1996; 96US-0609572.

AA (GEM)) GENETICS INST INC.

PI Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
PI Wood C;

AA
DR WPI: 1997-448632/41.

DR N-PSDB; AAT75213

aa New nucleic acid encoding interleukin-13 receptor binding chain and
 pt transformed cells - proteins, antibodies and inhibitors, for
 pt treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 pt and in diagnosis
 pt

PS Claim 11; Pages 30-31; 49pp; English.

The present sequence represents the murine interleukin-13 (IL-13) binding chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a mediator of the known biological activities of IL-13. Recombinant IL-13bc proteins, and antibodies raised against them, are used to inhibit the binding of IL-13 to its receptor. They are particularly used to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex disorders, especially lupus, nephritis, thyroiditis and Grave's disease. They are also used to treat immune deficiency (particularly in haematopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in vaccination. To potentiate IL-13 activity, a protein with such activity is combined with IL-13bc and the mixture applied, *in vivo*, to a cell expressing at least one chain of the IL-13 receptor other than IL-13bc. IL-13bc can also be used in diagnosis to detect expression of IL-13, its receptor or binding chain, and to raise specific antibodies which may be useful for treating some tumours.

AA	Sequence	383 AA;
SQ		

Query Match	58.1%	Score 1194.5;	DB 18;	Length 383;
Best Local Similarity	58.9%	Pred. No. 3e+108;		
Matches 219;	Conservative	55;	Mismatches 91;	Indels 7;
Gaps				

QY 1 MAFVCLAIGCLYTFLISTFGCTSSSDTEIKVNPQDFEIVDPGYLYLOWQPPLSLD 60

Db 1 mafv--hircfllctitgys---leikvnppqdfieildpallgylqlwkppvvie 54

QY 61' HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ 120

[illegible]

1. *Chlorophyll a* (Chl *a*)

QY IZI SSWAETTYWISPGQIPEIRKQDMDCVYNNWQYLLCSWRPGIGVLLDTNYNLFYWYEGLDH 180

Db I15 spwieasyglsdegsl etki qdmkci yynwqy lvcswkpgktvysdtnytmriwyegldh 1/4

QY 181 ALQCVDYIKADGQNI GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNI VKPLP 240QY

Db 175 alqcadylqhdekngcklsnldssdykdficvngssklepirssytvfqlgnivkplp 234

Case	Year	Age	Sex	Occupation	Education	Marital Status	Religion	Political Party	Income	Health	Family Size	Home Ownership	Auto Ownership	Life Insurance	Retirement	Charitable Contributions	Volunteer Work	Community Involvement	Life Satisfaction	Overall Well-being
1	2015	35	Male	Software Engineer	High School	Married	Catholic	Republican	\$75,000	Good	2	Owns	Owns	Yes	401k	\$100	Yes	Yes	8.5	9.0
2	2016	42	Female	Teacher	College	Single	Protestant	Democrat	\$50,000	Fair	1	Rents	Does Not Own	No	None	\$0	No	No	7.0	7.5
3	2017	28	Male	Marketing Executive	College	Married	Jewish	Democrat	\$90,000	Excellent	3	Owns	Owns	Yes	401k	\$200	Yes	Yes	9.0	9.5
4	2018	55	Female	Retired	High School	Married	Catholic	Republican	\$30,000	Poor	4	Owns	Owns	No	None	\$0	No	No	6.0	6.5
5	2019	30	Male	Entrepreneur	College	Single	Muslim	Democrat	\$120,000	Good	1	Owns	Owns	Yes	401k	\$500	Yes	Yes	9.5	10.0

[illegible]

00 233 p e i t n t s v e i s t a i t m k w s c p g g p i p p r c y t e l v i r e q u i s w e s a t c k n d m k i k r a n e z 291

QY JUC INQLCFVAKSANTIC
: ||| | ||||

Db 295 sedlcffvrckvniyc

RESULT 15

AAV95295
ID AAV95295 standard; Protein; 383 AA.

XX AC AAV95295;

XX DT 12-SEP-2000 (first entry)

XX DE IL-13 binding chain of mouse IL-13 receptor.

XX KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; antiallergic;
KW antiinflammatory; antiasthmatic; vaccine.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Peptide 1..21

FT /note= "signal peptide"

FT Protein 22..383

FT /note= "mature protein"

FT Domain 22..334

FT /note= "extracellular domain; a polypeptide
comprising amino acids 22-334 is
specifically claimed in Claim 11(b)"

FT Domain 335..356

FT /note= "transmembrane domain"

FT Domain 357..383

FT /note= "intracellular domain; a polypeptide
comprising amino acids 257-383 is
specifically claimed in Claim 11(c)"

XX PN WO200036103-A1.

XX XX 22-JUN-2000.

XX PF 13-DEC-1999; 99WO-US29493.

XX PR 14-DEC-1998; 98US-0211335.

XX PA (GENY) GENETICS INST INC.

XX PA (UYJO) UNIV JOHNS HOPKINS.

XX PI Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;

XX PI Wills-Karp M;

XX XX WPI; 2000-431587/37.

XX DR N-PSDB; AAA27911.

XX XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
asthma, Grave's disease and inflammatory conditions of the lung -

XX PS Claim 11(a); Page 50-51; 60pp; English.

XX XX The present sequence is that of the interleukin-13 binding chain
(IL-13bc) of the murine IL-13 receptor, as deduced from an isolated
C3H/HeJ mouse thymus cDNA clone (see AAA27911). IL-13bc is a member
of the haematopoietin receptor family that acts as a mediator of
IL-13. The invention provides methods for the recombinant
production of IL-13bc polypeptides, including claimed full-length
IL-13bc, its extracellular domain, and its intracellular domain.
IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
and IL-13 receptor inhibitors (e.g. antagonists of the interaction
of IL-13 and its receptor) can be used to treat conditions in
which IL-13 is implicated, particularly IgE-mediated conditions and
diseases including atopy, allergy, asthma, immune complex diseases
(e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
thyroiditis and Grave's disease), lung inflammation,
immunodeficiency, and cancer. Since IL-13 inhibits macrophage
activation, IL-13bc proteins can also be used to enhance macrophage

CC activation, e.g. in vaccination, treatment of mycobacterial or
CC intracellular organisms or parasite infections. IL-13bc proteins
CC may also be used to potentiate the effects of IL-13 in vitro and
CC in vivo, as diagnostic agents, and to screen for agents capable of
CC binding to IL-13bc or IL-13 receptor, or which interfere with the
CC binding of IL-13 to its receptor.

XX SQ Sequence 383 AA;

Query Match 58.1%; Score 1194.5; DB 21; Length 383;
Best Local Similarity 58.9%; Pred. No. 3e-108;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

OY 1 MAFVCLATGCLYTLFLISTFGCTSSSDTEIKVNPQDFEIVDPGVLGVLYLQWQPPLSLD 60
DB 1 mafv--hircicflilctitgys----leikvnpqdfelidpgllglylqwkppvvie 54
OY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLKNKGIEAKTHTLLPWQCTNGSEVQ 120
DB 55 kfgctleyelkyrnvdswkltitrlniykdgfdlnkgiegkirthlsehctngsevg 114
OY 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSWKPGLVLLDTNWNLFYWEGLDH 180
DB 115 spwleasygisdegslctkigdmkciyvnwqylvcswkpgktvysdtnymfwwyegidh 174
OY 181 ALQCVDYIKADGONIGCRFPVLEASDYKDYICVNGSSSENKPIRSSYTFQLQNTVKPLP 240
DB 175 alqcadyiqhdeknvgcklsnldssdykdficvngsklepirssytfvqlqnvkplp 234
OY 241 PVIYLTFTRESSCEIKLWKSIPGLPIPARCFDYEIREDDTTLVTATVENETTYTLKTNE 300
DB 235 peflhisvensidirmkwstpggpiprcycyeyelvireddiswesatdkndmklrrane 294
OY 301 TRQLCFVVRKVNIIYCDDGIWSEWSKQCEGEDLSKTKTLRFLWLPFGFILILVIFVTG 360
DB 295 sedlcfvrckvniycaddgiwsewseecwegygtgpdskil-fivpvcclffililllc 353
OY 361 LLRLRPNTYPKM 372
DB 354 livekeepeptl 365

Search completed: September 1, 2001, 19:07:03
Job time: 70 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:03 ; Search time 60.7 seconds
(without alignments)
342.570 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_343

Perfect score: 1901

Sequence: 1 MAFVCLAIAGLYFLISTTF.....EWSKQCEWGEDLSKTKTLR 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
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16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1901	100.0	380	18	Human interleukin-
2	1901	100.0	380	18	Human IL-13 bindin
3	1901	100.0	380	18	Human zcytor2 cyto
4	1901	100.0	380	19	Human HR-1 recepto
5	1901	100.0	380	19	Human cytokine/pep
6	1901	100.0	380	19	Homo sapiens HR-1
7	1901	100.0	380	21	IL-13 binding chai
8	1901	100.0	380	22	Human interleukin
9	1901	100.0	380	22	Human IL-13 recept
10	1875	98.6	380	18	Human zcytor2 cyto
11	1753	92.2	315	19	Mature interleukin

12	1753	92.2	359	19	AAW56260	Construct containi
13	1739	91.5	372	18	AAW36616	Celebus macaque Zc
14	1184	62.3	383	18	AAW35294	Murine IL-13 bindi
15	1184	62.3	383	21	AAW95295	IL-13 binding chai
16	1184	62.3	383	22	AAW72135	Murine interleukin
17	1184	62.3	383	22	AAW29747	Mouse IL-13 recept
18	456	24.0	157	19	AAW56252	Interleukin-13 bin
19	297	15.6	313	18	AAW21856	Protein used in pr
20	294.5	15.5	396	13	AAW22216	Sequence of human
21	294.5	15.5	396	13	AAW22220	Sequence of secret
22	294.5	15.5	420	13	AAW22219	Human interleukin-
23	294.5	15.5	420	19	AAW82842	Human IL-5 recepto
24	293.5	15.4	421	13	AAW25064	IL5-R-GFP 130 fusi
25	292.5	15.4	1026	16	AAW70121	Soluble human IL-5
26	292	15.4	335	13	AAW25063	shIL-5R-alpha. Sy
27	292	15.4	335	14	AAW33699	Sequence of human
28	289.5	15.2	420	13	AAW22215	Mouse interleukin-
29	287.5	15.1	426	18	AAW09821	Human interleukin-
30	285	15.0	427	18	AAW24973	Human interleukin-
31	285	15.0	427	22	AAW19807	IL-13/IL-4 dual tr
32	285	15.0	793	21	AAW92208	Human interleukin-
33	284	14.9	426	18	AAW09822	IL-13/IL-4 dual tr
34	284	14.9	784	21	AAW92207	Human interleukin-
35	283	14.9	427	22	AAW19808	Sequence of interl
36	230	12.1	398	13	AAW22212	Sequence of interl
37	229	12.0	315	13	AAW22214	Sequence of interl
38	229	12.0	332	13	AAW22213	Sequence of interl
39	229	12.0	332	13	AAW22218	Sequence of interl
40	229	12.0	415	13	AAW22211	Sequence of interl
41	229	12.0	415	13	AAW22217	Human cytokine rec
42	209	11.0	482	19	AAW31646	IL-2 receptor gamm
43	208	10.9	369	15	AAW47148	Fusion polypeptide
44	208	10.9	691	21	AAW92202	Fusion polypeptide
45	208	10.9	694	21	AAW92201	

ALIGNMENTS

RESULT 1

AAW24972 ID AAW24972 standard; protein; 380 AA.

XX AC AAW24972;

XX DT 22-JUN-1998 (first entry)

XX DE Human interleukin-13 beta receptor.

XX KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.

XX OS Homo sapiens.

XX PN WO9720926-A1.

XX PD 12-JUN-1997.

XX PF 07-NOV-1996; 96WO-FR01756.

XX PR 06-DEC-1995; 95FR-0014424.

XX PA (SNFI) SANOFI SA.

XX PI Caput D, Ferrara P, Laurent P, Vita N;

XX DR WPI; 1997-319773/29.

XX DR N-PSDB; AAT85826, AAT86464.

XX PT New purified human interleukin-13 receptors - and related nucleic

XX PT acids, useful for diagnosis and treatment of inflammation, allergy,

XX PS Claim 1; Figure 2a; 83pp; French.

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are designated for interleukin-13 (IL-13); the 380
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R beta
 CC and alpha which can be used as IL-13 antagonists, specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for gene
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunoassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFVCLAIGCLYTLFTTFCGCTSSDTEIKVNPQPQDFEIVDPGVLGYLQWPPPLSLD 60
 DB 1 mafvclaigcllytlfttfcgctssdteikvnpqpqdfeidvdpvglylylqwpplsl 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNKGEAKIHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynrigsetwktititknlykdgfdlnkgeakihltllpwqctngsevq 120
 QY 121 SSWAETTYWISPGQIPETKVDMDCVYNNQYLLCSWKPGIGVLLDYNLNFYWEGLDH 180
 DB 121 sswaettywispgqipetkvdmdcvynnyqyllcswkpgigvlldntnynlfywegldh 180
 QY 181 ALQCVDYIKADGQNIKGRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
 DB 181 alqcvdyikadgqnigrfpyleasdykdfyicvngsenkpirssyftfqlnkvkplp 240
 QY 241 PVYLTFRESSECEIKLWSIPGLPIPARCFDYEIEIREDDDTLTATVENETYLKTNE 300
 DB 241 pvytlftressceiklwsipglpiparcfdyeieiredddtltatvenetytlktne 300
 QY 301 TROLCFVVRKVNITYCSDGIGWSEWSDKQCWGEDLSKKTLLR 343
 DB 301 trqlcfvvrskvnitycsdgiwsewskqcwgedlskktllr 343

RESULT 2
 ID AAW35295 standard; Protein; 380 AA.
 XX AAW35295;
 AC AAW35295;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Human IL-13 binding chain of the IL-13 receptor.
 XX
 KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25

FT /label= signal_sequence
 FT /note= "putative"
 FT Protein 26..380
 FT /label= mature_protein
 FT Domain 26..341
 FT /label= extracellular_domain
 FT Domain 342..362
 FT /label= transmembrane_domain
 FT Domain 363..380
 FT /label= intracellular_domain
 XX
 PN W09731946-A1.
 XX
 PD 04-SEP-1997.
 XX
 PF 28-FEB-1997; 97WO-US03124.
 XX
 PR 01-MAR-1996; 96US-0609572.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;
 PI
 DR WPI; 1997-448632/41.
 DR N-PSDB; AAT95214.
 XX
 PT New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transforming cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis
 XX
 PS Claim 11; Pages 34-35; 49pp; English.
 XX
 CC The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied,
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating tumours.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTTFCGCTSSDTEIKVNPQPQDFEIVDPGVLGYLQWPPPLSLD 60
 DB 1 mafvclaigcllytlfttfcgctssdteikvnpqpqdfeidvdpvglylylqwpplsl 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNKGEAKIHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynrigsetwktititknlykdgfdlnkgeakihltllpwqctngsevq 120
 QY 121 SSWAETTYWISPGQIPETKVDMDCVYNNQYLLCSWKPGIGVLLDYNLNFYWEGLDH 180
 DB 121 sswaettywispgqipetkvdmdcvynnyqyllcswkpgigvlldntnynlfywegldh 180
 QY 181 ALQCVDYIKADGQNIKGRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
 DB 181 alqcvdyikadgqnigrfpyleasdykdfyicvngsenkpirssyftfqlnkvkplp 240

Qy 241 PVYLTFTRESSCEIKLWSIPGLPIPARCFDYIEIREDDTTLVTATVENETYLKTTNE 300
 Db 241 pvyitftressceiklwsipglpiparcfdyieireddtltvtatvenetylktne 300
 Qy 301 TRQLCFVVRVKVNIYCSDDGIWSEWSKQCWEGEDLSKKTLLR 343
 Db 301 trqicfvvrsvknlycsddgiwsewskqcwgedlskktllr 343

RESULT 3

AAW36613
 ID AAW36613 standard; Protein; 380 AA.

XX AC AAW36613;

DT 30-MAR-1998 (first entry)

XX Human Zcytor2 cytokine receptor protein.

XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 KW infertility; antagonist; contraceptive; diagnostic; therapeutic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Domain 340..363
 FT /label= transmembrane_domain
 FT Domain 364..380
 FT /label= intracellular_domain
 FT Domain 25..339
 FT /label= ligand_binding_domain

XX WO9733913-A1.

XX PD 18-SEP-1997.

XX PF 12-MAR-1997; 97WO-US04043.

XX PR 13-MAR-1996; 96US-0013345.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FU;
 PI O'Hara PJ;

XX WPI: 1997-470820/43.
 DR N-PSDB; AAT96782.

XX New nucleic acid encoding testis-specific cytokine receptor - useful
 PT for identification of ligands or antagonists, potentially for use as
 PT male contraceptives or for infertility treatment

XX PS Claim 2; Page 47-48; 79pp; English.

XX This sequence represents a novel ligand-binding receptor, Zcytor2,
 CC which shares homology with cytokine receptors and was isolated from human
 CC placental polyA+ RNA. The resulting polypeptide is a receptor for
 CC cytokines (particularly interleukin-13) and is expressed on the surface
 CC of testicular cells, probably being involved in spermatogenesis. It can
 CC be used to detect ligands that promote proliferation and/or
 CC differentiation of such cells in cultures and may also be used to treat
 CC infertility. Antagonists of this receptor may be used to characterise
 CC ligand-receptor interactions and as male-specific contraceptives. By
 CC blocking the action of IL-13, receptor antagonists and ligand-binding
 CC this receptor can also be used to modulate immune function, e.g. in
 CC allergy and asthma, as a diagnostic to determine circulating levels of
 CC ligand and also to isolate and purify ligands. Antibodies can be used to
 CC assay circulating receptor (an abnormal level may be indicative of
 CC disease such as cancer), for labelling cells that express the receptor,
 CC and therapeutically as antagonist.

XX Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTFELISTTFCGTSSTSSDTEIKVNPQQDFEIVDPGVLGYLYLQWOPPLSLD 60
 Db 1 mafvclaigcltyflisttfgctsssdteikvnpqqdfeiwdpgylylylqwpplslid 60
 Qy 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHITLLPWOCTNGSEVQ 120
 Db 61 hfkectveyelkyrnigsetwktititknlykdgfdlnkgeakihitllpwoctngsevg 120
 Qy 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSNKPGGIVLLDTNINLFYNYEGLDH 180
 Db 121 sswaettywispgipetkvqdmcdcvynwqyllcsnkp9igvlltdnynlfywyegldh 180
 Qy 181 ALQCVDYIKADQONIGCRFPYPYLEASDYKDYICVNGSENKPIRSSYFTFOLQIVKPLP 240
 Db 181 alqcvdyikadqonigcrfypyleasdykdyicvngssenkiprissyftfqlqivkplp 240
 Qy 241 PVYLTFTRESSCEIKLWSIPGLPIPARCFDYIEIREDDTTLVTATVENETYLKTTNE 300
 Db 241 pvyitftressceiklwsipglpiparcfdyieireddtltvtatvenetylktne 300
 Qy 301 TRQLCFVVRVKVNIYCSDDGIWSEWSKQCWEGEDLSKKTLLR 343
 Db 301 trqicfvvrsvknlycsddgiwsewskqcwgedlskktllr 343

RESULT 4

AAW41520
 ID AAW41520 standard; Protein; 380 AA.

XX AC AAW41520;

DT 22-JUN-1998 (first entry)

XX Human HR-1 receptor.

XX KW HR-1 receptor; human; cytokine; infection; asthma; allergy;
 KW haematopoietic disorder; tumour; therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Sig_peptide
 FT Protein 22..380
 FT /label= Mat_protein

XX WO9747741-A1.

XX PD 18-DEC-1997.

XX PF 12-JUN-1996; 96WO-US10262.

XX PR 12-JUN-1996; 96WO-US10262.

XX PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Appelbaum ER, Hu J;

XX WPI: 1998-052308/05.

XX DR N-PSDB; AAV04131..

XX PT Nucleic acid sequence encoding human cytokine peptide hormone
 PT receptor - useful to treat, prevent or diagnose, e.g. lowered
 PT resistance to infection, asthma, allergy or haematopoietic disease

XX PS Claim 13; Page 62-64; 76pp; English.

CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated the HR-1 receptor, that shows 27% identity
 CC and 52% similarity to the interleukin-5 receptor. Its amino acid
 CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
 CC human testis library. Recombinant HR-1 receptor can be expressed
 CC in claimed host cells, and used in a claimed method for identifying
 CC compounds which bind to, and activate or inhibit, it. HR-1
 CC receptor activators and agonists can be used to treat, prevent or
 CC diagnose predisposition to lowered resistance to infection, asthma,
 CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
 CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer.
 CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
 CC be used to treat conditions associated with HR-1 receptor
 CC overexpression. The antibodies can also be used to determine HR-1
 CC receptor levels, since overexpression may be diagnostic of tumours.
 XX Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTTGTCTSSSTETKVNPPQDFEIVDPGILYLYLQWPPPLSLD 60
 DB 1 mafvclaigcllytlsttgtctssstetkvnppqdfelvdpqylglylylqwppplsl 60
 QY 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynigsetwktitknlnhykgfdlنگكieakihltllpwqctngsevq 120
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLCSKPGIGVLLDTNLYNLFYWEGLDH 180
 DB 121 sswaetywispqgipetkvqdmcdvynnwqylcswkpgigvlltdnlnlyfywegl 180
 QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQQLQNVKPLP 240
 DB 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkiprissyftfqlqnvkplp 240
 QY 241 PVIYLTFTRESSCEIKLWSPILGPPIPARCFDYEIREDDTTLVTATVENETYLKTTNE 300
 DB 241 pviyltfressceiklwspilgpiiparcfdyeireddttlvtatvenetytlktne 300
 QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQCEWGEDLSKKTLLR 343
 DB 301 trqlcfvvrskvniycsddgiwsewsdkqcewedlskktllr 343

RESULT 5
 ID AAW41502
 AC AAW41502 standard; Protein; 380 AA.
 XX AAW41502;
 XX 08-JUN-1998 (first entry)
 DT Human cytokine/peptide receptor, HR-1 receptor.
 DE
 XX
 XX HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
 KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
 KW neutropenia; therapy.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Sig_peptide
 FT 22..380
 FT /label= Mat_protein
 FT /note= "Claim 14"
 XX
 PN EP812913-A2.
 XX

PD 17-DEC-1997.
 XX
 PF 04-JUN-1997; 97EP-0303815.
 XX
 PR 12-JUN-1996; 96US-0017843.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Appelbaum ER, Hu J;
 XX
 DR WPI; 1998-034974/04.
 DR N-PSDB; AAV04075.
 XX
 PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
 PT increase resistance to infections in individuals with trauma and/or
 PT burns
 XX
 PS Claim 13; Page 27-28; 34pp; English.

CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated HR-1 receptor. The amino acid sequence
 CC was deduced from a cDNA clone (see AAV04075) isolated from a human
 CC testis cDNA library. It shows 27% amino acid identity and 52%
 CC similarity with the human interleukin-5 receptor. Also claimed are
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an
 CC agonist to the polypeptide, antibody against the polypeptide, an
 CC antagonist that inhibits the activity of the polypeptide, a process
 CC for diagnosing a disease, or a susceptibility to disease, related
 CC to expression of HR-1 receptor, and a method for identifying
 CC compounds that activate or inhibit the HR-1 receptor. HR-1
 CC receptor protein and polynucleotides can be used for research,
 CC biological, diagnosis and (gene) therapy applications, e.g. to
 CC increase resistance to infections in individuals with trauma and/or
 CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
 CC predisposition to asthma, allergic disorders or disorders of
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
 CC cyclic neutropenia or as a consequence of cytotoxic therapy of
 CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLSTTGTCTSSSTETKVNPPQDFEIVDPGILYLYLQWPPPLSLD 60
 DB 1 mafvclaigcllytlsttgtctssstetkvnppqdfelvdpqylglylylqwppplsl 60
 QY 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynigsetwktitknlnhykgfdlنگكieakihltllpwqctngsevq 120
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLCSKPGIGVLLDTNLYNLFYWEGLDH 180
 DB 121 sswaetywispqgipetkvqdmcdvynnwqylcswkpgigvlltdnlnlyfywegl 180
 QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQQLQNVKPLP 240
 DB 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkiprissyftfqlqnvkplp 240
 QY 241 PVIYLTFTRESSCEIKLWSPILGPPIPARCFDYEIREDDTTLVTATVENETYLKTTNE 300
 DB 241 pviyltfressceiklwspilgpiiparcfdyeireddttlvtatvenetytlktne 300
 QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQCEWGEDLSKKTLLR 343
 DB 301 trqlcfvvrskvniycsddgiwsewsdkqcewedlskktllr 343

RESULT 6

AAW33603
ID AAW33603 standard; Protein; 380 AA.

XX
AC AAW33603;

XX
DT 08-JUN-1998 (first entry)

XX
DE Homo sapiens HR-1 receptor.

XX
KW Cytokine; hormone receptor; AIDS; acquired immune deficiency;
syndrome; aplastic anaemia; neutropaenia; cancer treatment;
infection resistance; diagnosis; tumours; HR-1 receptor;
asthma; allergic; haematopoietic; disorder.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Peptide I..21
FT /note= "signal peptide"

XX
PN WO9747742-A1.

XX
PD 18-DEC-1997.

XX
PF 09-JUL-1996; 96WO-US11459.

XX
PR 12-JUN-1996; 96WO-US10262.

XX
PR 12-JUN-1996; 96US-0017843.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
PI Appelbaum ER, Hu J;

XX
DR WPI; 1998-052309/05.

XX
DR N-PSDB; AAV02295.

XX
PT DNA encoding human cytokine-peptide hormone receptor - useful for
treating preventing or diagnosing, e.g. lowered resistance to
infection, asthma, allergy, or haematopoietic disease

XX
PS Claim 15; Fig 1; 75pp; English.

XX
CC The sequence is that of the human cytokine/peptide hormone receptor
(HR-1 receptor). This, or it's activators or agonists, can be used to
treat, prevent or diagnose predisposition to lowered resistance to
infection, asthma, allergic or haematopoietic disorders, e.g. where
induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
neutropaenia or cytotoxic treatments for cancer. Antagonists of the
receptor, e.g. antibodies or fragments of it may be used to treat
conditions associated with overexpression of the HR-1 receptor, e.g.
those listed above. Antibodies may also be used to assay levels of HR-1
receptor, overexpression of which may be diagnostic of tumours, by usual
immunoassays; to isolate and identify HR-1 receptor-expressing cells; or
for affinity purification of the HR-1 receptor.

XX
SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 4.6e-179;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGLYTFLISTTGTCTSSSTETKVPNPQDFEIVDPGLYGLYLQWPPPLSLD 60

DB 1 mafvclaiiglytflisttgtctssstetkvpnpqdfeidvpglylylqwpplsl 60

QY 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNKGEAKIHTLLPWQCTNGSEVQ 120

DB 61 hfkectveyelkynigsetwktititknlhykdgfdlnkgeakihltllpwqctngse 120

QY 121 SSWAETTYWISPGIPETKVDMDCVYNNWQYLCSWKPQIGVLLDTNLYNLFYWEGLDH 180

|||||

DB 121 sswaettywispgipetkvgmdcvynwqyllicswkpgigvlltdnynlfywegl 180
QY 181 ALQCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
DB 181 alqcvdylkadgqngicrfpyleasdykdfyicvngssenkprrssyftfqlqnvkplp 240
QY 241 PVLTFTRSSCEIKLKWISPLGPIPARCFDYEIEIREDDDTTLVTATVENETYTKTTNE 300
DB 241 pvlftfressceiklkwisplgpiparcfdeyeieiredddtltvtatvenetytkttne 300
QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQWEGEDLSKKTLRL 343
DB 301 trqlcfvvrskvniycsddgiwsewsdkqwegedlskktllr 343

RESULT 7

AA95296

ID AA95296 standard; Protein; 380 AA.

XX
AC AA95296;

XX
DT 12-SEP-2000 (first entry)

XX
DE IL-13 binding chain of human IL-13 receptor.

XX
KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
immune complex disease; lupus; nephritis; thyroiditis;
Grave's disease; inflammatory; infection; therapy; anti-allergic;
anti-inflammatory; antiasthmatic; vaccine.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT Peptide I..25

FT /note= "signal peptide"

FT Protein 26..380

FT /note= "mature protein"

FT Domain 26..341

FT /note= "extracellular domain; a polypeptide
comprising amino acids 22-334 is
specifically claimed in Claim 11(e)"

FT Domain 342..362

FT /note= "transmembrane domain"

FT Domain 363..380

FT /note= "intracellular domain; a polypeptide
comprising amino acids 237-383 is
specifically claimed in Claim 11(f)"

XX
PN WO200036103-A1.

XX
PD 22-JUN-2000.

XX
PF 13-DEC-1999; 99WO-US29493.

XX
PR 14-DEC-1998; 98US-0211335.

XX
PA (GEMY) GENETICS INST INC.

XX
PA (UYJO) UNIV JOHNS HOPKINS.

XX
PI Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
Wills-Karp M;

XX
DR WPI; 2000-431587/37.

XX
DR N-PSDB; AAA27912.

XX
PT New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
asthma, Grave's disease and inflammatory conditions of the lung -
Claim 11(d); Page 53-54; 60pp; English.

XX
CC The present sequence is that of the interleukin-13 binding chain

CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated
 CC human testis cDNA clone (see AAA27912). IL-13bc is a member of
 CC the haematopoietin receptor family that acts as a mediator of
 CC IL-13. The invention provides methods for the recombinant
 CC production of IL-13bc polypeptides, including claimed full-length
 CC IL-13bc, its extracellular domain, and its intracellular domain.
 CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
 CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
 CC of IL-13 and its receptor) can be used to treat conditions in
 CC which IL-13 is implicated, particularly IgE-mediated conditions and
 CC diseases including atopy, allergy, asthma, immune complex diseases
 CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
 CC thyroiditis and Grave's disease), lung inflammation,
 CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
 CC activation, IL-13bc proteins can also be used to enhance macrophage
 CC activation, e.g. in vaccination, treatment of mycobacterial or
 CC intracellular organisms or parasite infections. IL-13bc proteins
 CC may also be used to potentiate the effects of IL-13 in vitro and
 CC in vivo, as diagnostic agents, and to screen for agents capable of
 CC binding to IL-13bc or IL-13 receptor, or which interfere with the
 CC binding of IL-13 to its receptor.
 XX
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 21; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTFGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
 Db 1 mafvclaigcllytlstftgctssdteikvnpqdfvdpgylylqwqpplsl 60
 QY 61 HFKECTVEYELKYNIGSEWTKTIITKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktititknlhkydgfdlنگkieakihllpwqctngse 120
 QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNMYNLFYWEGLDH 180
 Db 121 sswaetywispogipetkvqdmcdvynnyqyllcswkpgigvllدtnmynlfywegldh 180
 QY 181 ALCQVDYIKADQNGICRFFYLEASDYKDFYICVNGSSENKPIRSSFTFQLOINVRPLP 240
 Db 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkprrsftfqlnivrplp 240
 QY 241 PVIYLTFTRESSCEIKLWSIPLGPIPARCFDYETEIREDDTTLVTAVENETYLKTTNE 300
 Db 241 pviylftressceiklwsiplgpiparcfdyeteireddttlvtatvenetylktne 300
 QY 301 TRQLCFVVRKVNITYCSDDGTSWSDSKQWEGEDLSKKTLLR 343
 Db 301 trqlcfvvrskvnitycsddgtswsdskqcwgedlskktllr 343

RESULT 8

AA72136
 ID AAY72136 standard; Protein; 380 AA.

XX
 AC AAY72136;

XX 24-APR-2001 (first entry)

XX Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
 XX Human; IL-13; interleukin-13 binding chain of IL-13 receptor; IL13bc;
 KW therapy; tissue fibrosis; Schistosoma infection; surgical incision;
 KW cytostatic; wound; IL-13 related condition; allergic condition;
 KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;
 KW macrophage activation.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25
 FT /label= signal_peptide
 FT Region 1..81
 FT /note= "this region is identical to the translated
 FT sequence of an expressed sequence tag (EST) identified
 FT as Y999f10.r1 human cDNA clone 41648 5"
 FT Protein 26..380
 FT /label= Mature_human_interleukin (IL)-13_binding_chain_
 FT of_IL-13_receptor
 FT Domain 26..341
 FT /note= "Extracellular domain; this region is specifically
 FT claimed in claims 1e, 6e, 15e and 23e"
 FT Domain 342..362
 FT /note= "transmembrane domain"
 FT Domain 363..380
 FT /note= "Intracellular domain; this region is specifically
 FT claimed in claims 1f, 6f, 15f and 23f"

WO200078336-A1.

28-DEC-2000.

21-JUN-2000; 2000WO-US17103.

21-JUN-1999; 99US-0334512.

(GEMY) GENETICS INST INC.
 (UYJO) UNIV JOHNS HOPKINS.

Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 Wills-Karp M;

WPI: 2001-080753/09.

N-PSDB; AAD02335.

Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
 in a mammalian subject, involves administering a pharmaceutical
 composition comprising IL-13 antagonist -

Claim 1a; Page 69-70; 72pp; English.

The invention relates to a method of treating, or inhibiting
 the formation of tissue fibrosis in mammals, which involves
 administering a pharmaceutical composition comprising interleukin
 (IL)-13 antagonist. The protein of the invention is useful for
 treating tissue fibrosis resulting from infection with Schistosoma
 or from healing of a wound which is a surgical incision, or
 inhibiting formation of tissue fibrosis which affects tissues such
 as liver, skin epidermis and endodermis, muscle, tendon, cartilage,
 cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
 testis, ovary, adrenal gland, artery, vein, colon, small intestine,
 biliary tract and gut. It is also used in the treatment or modulation
 of various IL-13 related conditions such as allergic conditions,
 CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.
 CC The present sequence is human interleukin (IL)-13
 CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used
 CC to potentiate the effects of IL-13. This protein is also used to
 CC enhance macrophage activation and hence can be used in vaccination
 CC or treatment of mycobacterial or parasitic infections.

XX Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 4.6e-179;
 Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTFGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
 Db 1 mafvclaigcllytlstftgctssdteikvnpqdfvdpgylylqwqpplsl 60
 QY 61 HFKECTVEYELKYNIGSEWTKTIITKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
 Db 1 hfkectveyelkynigsetwktititknlhkydgfdlنگkieakihllpwqctngse 120

Db 61 hfkectveyelkyrnigsetwktiitknlhkygdgfdlnkgeakihltllpwqctngsevg 120

Qy 121 SSWAETTYWISPGIPETKVDMDCVYVNWQYLLCSWRPGIGVLLDTNYNLFYWYEGLDH 180
 |||||

Db 121 sswaettywispgipetkvqmdcvyynwqyllcswkpgigvllidtnynlfywyegldh 180
 |||||

Qy 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQIQNVKPLP 240
 |||||

Db 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkprrsyttfqlqnvkplp 240
 |||||

Qy 241 PVLFTFTRESSCEIKLWSIPLGPPIPARCFDYEIEIREDDTTLVTATVENETYTLTKTNE 300
 |||||

Db 241 pvlftftressceiklwsiplgppiparcfdyeyeiireddttlvatvenetytltkttne 300
 |||||

Qy 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGEDLSKTKTLR 343
 |||||

Db 301 trqlcfvvrsvkniycsddgiwsewsdkqcegedlskktllr 343
 |||||

RESULT 9

AAB29748

ID AAB29748 standard; Protein; 380 AA.

XX AC

XX AAB29748;

XX DT 23-FEB-2001 (first entry)

XX DE Human IL-13 receptor IL-13 binding chain (IL-13bc).

XX KW Human; IL-13 receptor; interleukin-13; IL-13 binding chain;

XX KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnery;

XX KW wound healing; schistosoma infection; liver; skin; muscle;

XX KW cartilage; cardiac tissue; lung tissue; uterine tissue;

XX KW intestinal tissue; vascular tissue; neural tissue.

XX OS Homo sapiens.

XX PN WO200064944-A1.

XX PD 02-NOV-2000.

XX PF 28-APR-2000; 2000WO-US11612.

XX PR 28-APR-1999; 99US-0301808.

XX PA (GEMY) GENETICS INST INC.

XX PI Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;

PI Whitters MJ, Wood C;

XX DR WPI; 2001-024676/03.

XX DR N-PSDB; AAC81416.

XX PT Treating or inhibiting tissue fibrosis resulting from infection with

PT schistosoma and wound healing involves administering interleukin-13 or

PT interleukin-4 antagonist

XX PS Claim 1; Page 76-77; 82pp; English.

XX CC The invention relates to a method of treating fibrosis in a mammal

CC by administering an interleukin-13 (IL-13) antagonist or an IL-4

CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding

CC chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or

CC soluble fragments thereof. The method is useful for treating or

CC inhibiting the formation of tissue fibrosis resulting from the healing

CC of a wound, including a surgical incision wound, or from infection with

CC schistosoma. The method may be used to treat fibrosis in a variety of

CC tissues, particularly liver tissue, but also skin epidermis, skin

CC endoderms, muscle, tendon, cartilage, cardiac tissue, pancreatic

CC tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,

CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut

CC tissue. The present sequence represents human IL-13bc.

SQ Sequence 380 AA;

Query Match 100.0%; Score 1901; DB 22; Length 380;

Best Local Similarity 100.0%; Pred. No. 4.6e-179; Indels 0; Gaps 0;

Matches 343; Conservative 0; Mismatches 0;

Qy 1 MAFVCLAIGCLYTLFISTTFCGTSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
 |||||

Db 1 mafvclaigcltyflisttfgctssdteikvnpqdfeiavdpvglylylqwqpplslid 60
 |||||

Qy 61 HFKECTVEYELKYRNIGSETWKTITKNLHYKDGFDLNGKEAKIHTLLPWQCTNGSEVQ 120
 |||||

Db 61 hfkectveyelkyrnigsetwktiitknlhkygdgfdlnkgeakihltllpwqctngsevg 120
 |||||

Qy 121 SSWAETTYWISPGIPETKVDMDCVYVNWQYLLCSWRPGIGVLLDTNYNLFYWYEGLDH 180
 |||||

Db 121 sswaettywispgipetkvqmdcvyynwqyllcswkpgigvllidtnynlfywyegldh 180
 |||||

Qy 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQIQNVKPLP 240
 |||||

Db 181 alqcvdyikadqngicrfyleasdykdfyicvngssenkprrsyttfqlqnvkplp 240
 |||||

Qy 241 PVLFTFTRESSCEIKLWSIPLGPPIPARCFDYEIEIREDDTTLVTATVENETYTLTKTNE 300
 |||||

Db 241 pvlftftressceiklwsiplgppiparcfdyeyeiireddttlvatvenetytltkttne 300
 |||||

Qy 301 TRQLCFVVRKSVNIYCSDDGIWSEWSKQCEGEDLSKTKTLR 343
 |||||

Db 301 trqlcfvvrsvkniycsddgiwsewsdkqcegedlskktllr 343
 |||||

RESULT 10

AAB36614

ID AAB36614 standard; Protein; 380 AA.

XX AC

XX AAB36614;

XX DT 30-MAR-1998 (first entry)

XX DE Human Zcytor2 cytokine receptor protein.

XX KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;

XX KW infertility; antagonist; contraceptive; diagnostic; therapeutic.

XX OS Homo sapiens.

XX PN WO9733913-A1.

XX PD 18-SEP-1997.

XX PF 12-MAR-1997; 97WO-US04043.

XX PR 13-MAR-1996; 96US-0013345.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;

PI O'Hara PJ;

XX DR WPI; 1997-470820/43.

XX DR N-PSDB; AAT96783.

XX PT New nucleic acid encoding testis-specific cytokine receptor - useful

PT for identification of ligands or antagonists, potentially for use as

PT male contraceptives or for infertility treatment

XX PS Claim 1; Page 51-53; 79pp; English.

XX CC This sequence represents a novel ligand-binding receptor, Zcytor2, which

CC shares homology with cytokine receptors and was isolated from a human

CC testis cDNA library. The resulting polypeptide is a receptor for

CC cytokines (particularly interleukin-13) and is expressed on the surface

of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor, and therapeutically as antagonist.

Sequence 380 AA;

Query Match 98.6%; Score 1875; DB 18; Length 380;
Best Local Similarity 99.1%; Pred. No. 1.7e-176;
Matches 340; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTGCTSSDTEIKVNPDPDFEIVDPGVLYLQWOPPLSLD 60
DB 1 mafvclaigcllytlftstgctssdteikvnpdpdfEIVDPGVLYLQWOPPLSLD 60
QY 61 HFKECTVEYELKYNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
DB 61 hfkeytveyelkynigsetwktitiknlhykdgfdlnkgieakihtllpwqctngseVq 120
QY 121 SSWAETTWISPOGIPETKVDQMDCVYNNWQYLLCSWKPFGIGVLLDTNLYFWYEGLDH 180
DB 121 sswaettywispogipetkvqmdcvvynwqyllcswkpgigvlldtynlfwyegidl 180
QY 181 ALQCVDYIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKVRPLP 240
DB 181 alqcvdyikadqonigcrfyleasdykdfyicvngssenkiprissyftfqlqnlvklp 240
QY 241 PVLFTTRESSCEIKLWSIPGLPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE 300
DB 241 pvlfttressceiklkwipglpiparcfdyeiEIREDDTTLvtatvenetytlktTne 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGEDLSKKTLLR 343
DB 301 trqlcfvvrskvniycsddgiwsewsdkqcegedlskktllr 343

RESULT 11
AAW56261
ID AAW56261 standard; Protein; 315 AA.
XX
AC AAW56261;
XX
DT 16-SEP-1998 (first entry)
XX
DE Mature interleukin-13 binding protein.
XX
KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.
XX
OS Homo sapiens.
XX
PN W09810638-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-AU00591.
XX
PR 27-FEB-1997; 97AU-0005374.
XX
PR 10-SEP-1996; 96AU-0002262.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX

DR WPI; 1998-207062/18.
DR N-PSDB; AAV22702.
XX
PT New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX
PS Disclosure; Page 55-56; 69pp; English.
XX
CC The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.

XX Sequence 315 AA;

Query Match 92.2%; Score 1753; DB 19; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPDPDFEIVDPGVLYLQWOPPLSLDHFKECTVEYELKYNIGSETWKTITIKN 88
DB 1 eikvnpdpdfEIVDPGVLYLQWOPPLSLDHFKECTVEYELKYNIGSETWKTITIKN 88
QY 89 LHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQSSWAETTWISPOGIPETKVDQMDCVY 148
DB 61 lhykdgfdlnkgieakihtllpwqctngseVqsswaettywispogipetkvqmdcvy 120
QY 149 NWQYLLCSWKPFGIGVLLDTNLYFWYEGLDHALQCVDYIKADQONIGCRFPYLEASDYK 208
DB 121 nwqyllcswkpgigvlldtynlfwyegldhalqcvdyikadqonigcrfyleasdyk 180
QY 209 DFYICVNGSSSENKPIRSSYFTFOLQNIKVRPLPVLFTTRESSCEIKLWSIPGLPIPAR 268
DB 181 dfyicvngssenkiprissyftfqlqnlvklpvpvlttressceiklkwipglp 240
QY 269 CFDEIEIREDDTTLVTATVENETYTLKTTNETQLCFVVRSKVNIYCSDDGIWSEWSK 328
DB 241 cfdeieireddtTLvtatvenetytlktTnetqlcfvvrskvniycsddgiwseWsdK 300
QY 329 QCWEGEDLSKKTLLR 343
DB 301 qcwgedlskktllr 315

RESULT 12
AAW56260
ID AAW56260 standard; Protein; 359 AA.
XX
AC AAW56260;
XX
DT 16-SEP-1998 (first entry)
XX
DE Construct containing mature interleukin-13 binding protein.
XX
KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.
XX
OS Homo sapiens.
XX
PN W09810638-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-AU00591.
XX
PR 27-FEB-1997; 97AU-0005374.
PR 10-SEP-1996; 96AU-0002262.
XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
PI WPI; 1998-207062/18.
XX N-PSDB; AAV22701.
DR New isolated interleukin-13 binding protein - used to develop
XX products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
PT Example 14; Page 52-53; 69pp; English.
XX
XX The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX
XX Sequence 359 AA;
SQ
Query Match 92.2%; Score 1753; DB 19; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.6e-164;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 29 EIKVNPDDFEIVDPGGLYGLYQWQPLSLDHFKECTVEYELKYRNIGSETWKTIIITKN 88
Db 45 elkvnppqdfelvdpgylyglwqppslsdhfkectveyelkyrnigsetwktiiitkn 104
QY 89 LHYKDGFLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCVY 148
Db 105 lhykdgflnkgieakihllpwqctngsevsqswaettywispogipetkvqdmcdvyy 164
QY 149 NWQYLLCSWKGIGVLLDTNLFYWGGLHALQCVDIKADGONICRPFYLEASDYK 208
Db 165 nwqyllcswkpgigvlltdnlyfwyegldhalqcvdyikadgqngicrpfyleasdyk 224
QY 209 DFYICVNGSSENKPIRSSYFTFQLNIVKPLPPVYLTFTRESSCEIKLWSIPLGPIPAR 268
Db 225 dfyicvngssenkprrsyftfqlnkvkplppvyltftressceiklwsiplgpiPAR 284
QY 269 CFDEYIEIREDDTLTATVENETYLKTTNETROLCFWRSKVNIIYSDGIGSEWSDK 328
Db 285 cfdeyeireddtlvtatvenetyltktnetrolcfvrskvniiysdggigsewsdk 344
QY 329 QCWEGEDLSKTKLLR 343
Db 345 qcwegedlsktkllr 359
RESULT 13
AAW36616
ID AAW36616 standard; Protein; 372 AA.
XX AC AAW36616;
XX 30-MAR-1998 (first entry)
XX Celebus macaque Zcytor2 protein.
XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX Macaque sp.
XX Key Location/Qualifiers
FH 1..372
FT Protein /label- Zcytor2
FT /note- "partial protein sequence"
XX

PN WO9733913-A1.
XX 18-SEP-1997.
XX 12-MAR-1997; 97WO-US04043.
XX 13-MAR-1996; 96US-0013345.
XX (ZYMO) ZYMOGENETICS INC.
XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
PI O'Hara PJ;
XX WPI; 1997-470820/43.
DR N-PSDB; AAT96784.
XX New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
XX
XX Example 4; Page 56-57; 79pp; English.
PS This sequence represents a novel ligand-binding receptor, Zcytor2,
CC which shares homology with cytokine receptors and is isolated from
CC testis tissue obtained from a Celebus macaque. The resulting polypeptide
CC is a receptor for cytokines (particularly interleukin-13) and is
CC expressed on the surface of testicular cells, probably being involved in
CC spermatogenesis. It can be used to detect ligands promoting proliferation
CC and/or differentiation of such cells in cultures and may also be used to
CC treat infertility. Antagonists of this receptor may be used to
CC characterise ligand-receptor interactions and as male-specific
CC contraceptives. By blocking the action of IL-13, receptor antagonists and
CC ligand-binding this receptor can also be used to modulate immune
CC function, e.g. in allergy and asthma, as a diagnostic to determine
CC circulating levels of ligand and also to isolate and purify ligands.
CC Antibodies can be used to assay circulating receptor (an abnormal level
CC may be indicative of disease such as cancer), for labelling cells that
CC express the receptor, and therapeutically as antagonist.
XX
SQ Sequence 372 AA;
Query Match 91.5%; Score 1739; DB 18; Length 372;
Best Local Similarity 93.3%; Pred. No. 4.1e-163;
Matches 319; Conservative 5; Mismatches 18; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTLITFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYQWQPLSLD 60
Db 1 mafvylairclctflistftgystdsdteikvnpqdfelvdpgylyglwqppslsd 60
QY 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFLNKGIEAKIHTLLPWQCTNGSEVQ 120
Db 61 nfkectveyelkyrnigsetwtiitknhykdgfdlnkgieakihllpwqctngsevg 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSWKGIGVLLDTNLYNLFYWYEGLDH 180
Db 121 sswaettywispogipetkvqdmcdvynwqyllcswkpgigvlltdnlynfwyegldr 180
QY 181 ALOCVDYIKADGONICRPFYLEASDYKDFYICVNGSSENKPIRSSYFTFQLNIVKPLP 240
Db 181 alqcvdyikvqdgngicrpfyleasdykdfyicvngssenkprrsyftfqlnkvkplp 240
QY 241 PVLITFTRESSCEIKLWSIPLGPIPARCFDYEIREDDTLTATVENETYLKTTNE 300
Db 241 pvlitctqesyleiklwsiplgpiPARcfyeyeiREDDTLTATVENETYLKTTNE 300
QY 301 TRQLCFVVRKVNIIYSDGIGSEWSDKQWEGEDLSKTKLL 342
Db 301 trqlcfvvrskvniiysdggigsewsdkqcwegedlsktkll 342
RESULT 14
AAW35294

AAW35294 standard; Protein; 383 AA.
AAW35294;
27-MAR-1998 (first entry)
Murine IL-13 binding chain of the IL-13 receptor.
Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
allergy; asthma; immune complex disorder.
Mus sp.
Key Location/Qualifiers
Peptide 1..21
Protein /label= signal_sequence
22..383 /note= "putative"
Domain /label= mature_protein
22..334 /label= extracellular_domain
335..356 /label= transmembrane_domain
357..383 /label= intracellular_domain
WO9731946-A1.
04-SEP-1997.
28-FEB-1997; 97WO-US03124.
01-MAR-1996; 96US-0609572.
(GEMY) GENETICS INST INC.
Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
Wood C;
WPI; 1997-448632/41.
N-PSDB; AAT75213.
New nucleic acid encoding interleukin-13 receptor binding chain and
transformed cells - proteins, antibodies and inhibitors, for
treating immunoglobulin E-mediated diseases, e.g. Graves disease,
and in diagnosis
Claim 11; Pages 30-31; 49pp; English.
The present sequence represents the murine interleukin-13 (IL-13) binding
chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
mediator of the known biological activities of IL-13. Recombinant
IL-13bc proteins, and antibodies raised against them, are used to
inhibit the binding of IL-13 to its receptor. They are particularly used
to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
They are also used to treat immune deficiency (particularly in
haematopoietic progenitor cells), cancer etc., and to increase macrophage
activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
with such activity is combined with IL-13bc and the mixture applied,
in vivo, to a cell expressing at least one chain of the IL-13 receptor
other than IL-13bc. IL-13bc can also be used in diagnosis to detect
expression of IL-13, its receptor or binding chain, and to raise specific
antibodies which may be useful for treating some tumours.
Sequence 383 AA;
Query Match 62.3%; Score 1184; DB 18; Length 383;
Best Local Similarity 64.0%; Pred. No. 2.2e-108;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCLYTLSTFGCTSSDSTEIKVNPQDFEIVDPGYLYLQWQPPLSLD 60
DB 1 mafv--hircicfllctitgys----leikvnpqdfelidpgllgyllylqkppvvie 54
QY 61 HFKECTVEYELKYRNISETWKTIIITKLNHYKDGFDLKNKGIEAKIHTLLPWOCTNGSEVQ 120
DB 55 kfkgtleyelkyrnvdswkltiitrlniykdgfdlnkgiegkirthlsehtngsevg 114
QY 121 SSWAETTYWISPOGIPETKVDMDCVYVNWQYLLCSWPGVGLDNTNLYFWYWEGLDH 180
DB 115 spwleasygisdegslctikdmkciywnqyivcswpkgktvysdntymffwyegldh 174
QY 181 ALOQVDYIKADGONIGCRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNVKPLP 240
DB 175 alqcadyiqhdeknvgcklsnldssdykdficvngsklepirssytfqlqnvkplp 234
QY 241 PVIYLTFTRESSCEIKLWSIPLGPIPARCFDYEIFEIRDDTTLVATVENETTYTLTKTNE 300
DB 235 peflhisvensidrmkwstpggpiprcycyvelivreddiswesatdkndmklrrane 294
QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQCWEG 333
DB 295 sedlcfvrckvniycaddgiwsewseececweg 327
RESULT 15
AAW95295
ID AAW95295 standard; Protein; 383 AA.
XX AC AAW95295;
XX DT 12-SEP-2000 (first entry)
XX DE IL-13 binding chain of mouse IL-13 receptor.
XX KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
XX KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
XX KW immune complex disease; lupus; nephritis; thyroiditis;
XX KW Grave's disease; inflammatory; infection; therapy; antiallergic;
XX KW antinflammatory; antiasthmatic; vaccine.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
22..383
FT Domain /note= "mature protein"
22..334
FT /note= "extracellular domain; a polypeptide
comprising amino acids 22-334 is
specifically claimed in Claim 11(b)"
FT Domain 335..356
FT /note= "transmembrane domain"
FT Domain 357..383
FT /note= "intracellular domain; a polypeptide
comprising amino acids 257-383 is
specifically claimed in Claim 11(c)"
WO200036103-A1.
22-JUN-2000.
13-DEC-1999; 99WO-US29493.
14-DEC-1998; 98US-0211335.
(GEMY) GENETICS INST INC.
(UYJO) UNIV JOHNS HOPKINS.
Collins M, Donaldson D, Fitz L, Neben T, Whitters M, Wood C;
Wills-Karp M;
XX

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:08:36 ; Search time 35.33 Seconds
(without alignments)
199.901 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_343

Perfect score: 1901
Sequence: 1 MAFVCLAIGCLYTLFTLSTTF.....EWSDKOCWGEDLSKTKLLR 343

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1901	100.0	380	1	US-08-609-572-4
2	1901	100.0	380	4	US-08-841-751-4
3	1901	100.0	380	4	US-08-846-340-4
4	1184	62.3	383	1	US-08-609-572-2
5	1184	62.3	383	4	US-08-841-751-2
6	1184	62.3	383	4	US-08-846-340-2
7	294.5	15.5	420	1	US-07-757-390-13
8	294.5	15.5	420	1	US-08-442-282-13
9	294.5	15.5	420	1	US-08-442-281-13
10	294.5	15.5	420	2	US-08-939-727-13
11	293.5	15.4	396	1	US-07-757-390-14
12	293.5	15.4	396	1	US-08-442-282-14
13	293.5	15.4	396	1	US-08-442-281-14
14	293.5	15.4	396	2	US-08-939-727-14
15	293	15.4	313	3	US-08-836-561-106
16	292	15.4	335	1	US-07-947-130-2
17	292	15.4	335	1	US-08-421-822-2
18	292	15.4	335	1	US-08-421-823-2
19	285	15.0	427	4	US-08-969-125-9
20	229	12.0	315	1	US-07-757-390-8
21	229	12.0	315	1	US-08-442-282-8
22	229	12.0	315	1	US-08-442-281-8
23	229	12.0	315	2	US-08-939-727-8
24	229	12.0	332	1	US-07-757-390-7
25	229	12.0	332	1	US-08-442-282-7
26	229	12.0	332	1	US-08-442-281-7
27	229	12.0	332	2	US-08-939-727-7

Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 7, Appli
Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-08-609-572-4
; Sequence 4, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-609-572-4

Query Match 100.0%; Score 1901; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTLFTLSTTFGCTSSSDTEIKVNPQDFEIVDPGVLYLQWQPPLSLD 60

|||||
Db 1 MAFVCLAIGCLYTLSTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
QY 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKEAKIHTLLPQCINGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKEAKIHTLLPQCINGSEVQ 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSWPKGIGVLLDTNLYNFWYEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSWPKGIGVLLDTNLYNFWYEGLDH 180
QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQIQNIVKPLP 240
Db 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQIQNIVKPLP 240
QY 241 PVLFTFRESSCEIKLWSIPLGPIPARCFDYEIEIRDDTTLVTATVENETYLKTTNE 300
Db 241 PVLFTFRESSCEIKLWSIPLGPIPARCFDYEIEIRDDTTLVTATVENETYLKTTNE 300
QY 301 TRQLCFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLR 343
Db 301 TRQLCFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLR 343

RESULT 2
US-08-841-751-4
; Sequence 4, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/841.751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-841-751-4

Query Match 100.0%; Score 1901; DB 4; Length 380;

Best Local Similarity 100.0%; Pred. No. le-186;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTLSTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTLSTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
QY 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKEAKIHTLLPQCINGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKEAKIHTLLPQCINGSEVQ 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSWPKGIGVLLDTNLYNFWYEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSWPKGIGVLLDTNLYNFWYEGLDH 180
QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQIQNIVKPLP 240
Db 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQIQNIVKPLP 240
QY 241 PVLFTFRESSCEIKLWSIPLGPIPARCFDYEIEIRDDTTLVTATVENETYLKTTNE 300
Db 241 PVLFTFRESSCEIKLWSIPLGPIPARCFDYEIEIRDDTTLVTATVENETYLKTTNE 300
QY 301 TRQLCFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLR 343
Db 301 TRQLCFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLR 343

RESULT 3
US-08-846-340-4
; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-846-340-4

```
Query Match      100.0%; Score 1901; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLFISTTFCGCTSSSDTEIKVNPDPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTLFISTTFCGCTSSSDTEIKVNPDPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
Qy 121 SSWAETTWISPOGIPETKVDMDCVYNNQYLCSKPGIGVLLDTNYNLFYWEGLDH 180
Db 121 SSWAETTWISPOGIPETKVDMDCVYNNQYLCSKPGIGVLLDTNYNLFYWEGLDH 180
Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQLOIVKPLP 240
Db 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQLOIVKPLP 240
Qy 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLTKTNE 300
Db 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLTKTNE 300
Qy 301 TROLCFVVRKVNICYSDGDIWSEWSKQCEGDELKSKTLRL 343
Db 301 TROLCFVVRKVNICYSDGDIWSEWSKQCEGDELKSKTLRL 343

RESULT 4
US-08-509-572-2
; Sequence 2, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-609-572-2

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Query Match      62.3%; Score 1184; DB 1; Length 383;
Best Local Similarity 64.0%; Pred. No. 2e-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

Qy 1 MAFVCLAIGCLYTLFISTTFCGCTSSSDTEIKVNPDPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Db 1 MAFV--HRCICFLLCTITGYS----LEIKVNPDPQDFEILDPLGLGYLYLQWKPVPVIE 54
Qy 61 HFKECTVEYELKYNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
Db 55 KFKGCTLEYELKYNVSDSNKTIITRNLIYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114
Qy 121 SSWAETTWISPOGIPETKVDMDCVYNNQYLCSKPGIGVLLDTNYNLFYWEGLDH 180
Db 115 SPWIEASTGIDSGSLETKIQDMKCIYYNNQYLCSKPGKTVYSDTNYTFFWYEGLDH 174
Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQLOIVKPLP 240
Db 175 ALQCADYLQHEKNVGVCKLSNLDSSDYKDFYICVNGSSEKLEPIRSSYTFQLOIVKPLP 234
Qy 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLTKTNE 300
Db 235 PEFLHISVENSIDIRMKWSTFGGPIPPRCYTYEIVIREDDISWESATDKNDMKLRRANE 294
Qy 301 TROLCFVVRKVNICYSDGDIWSEWSKQCEG 333
Db 295 SEDLCFFVRKVNICYADDDGIWSEWSEECWEG 327

RESULT 5
US-08-841-751-2
; Sequence 2, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-841-751-2

Query Match 62.3%; Score 1184; DB 4; Length 383;
Best Local Similarity 64.0%; Pred. No. 2e-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPQDPFEIVDPGVLGYLYLQWQPPSLD 60
DB 1 MAFV--HIRCLCFILLCTITGYS-----LEIKVNPQDPFEILDGGLLYLQWQPPVIE 54

QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKTEAKIHTLLPWQCTNGSEVQ 120
DB 55 KFKGCTLEYELKYRNVDSDSWKTIITRNLIYKDGFDLNGKTEGKIRTHLSEHCTNGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPFGIGVLLDTNLYNLFYVVEGLDH 180
DB 115 SPWIEASVIGSDEGSLFKIQDMKCIYNNQYLLCSWKPFGITVSDNTYTFVVEGLDH 174

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFICVNGSSENKPIRSSYFTFOLQNVKPLP 240
DB 175 ALQCADYLQHDKNVCKLSNLDSSDYKDFICVNGSSKLEPIRSSYTFVQLOQNVKPLP 234

QY 241 PVIYLTFTRESCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNE 300
DB 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDKMLKRRANE 294

QY 301 TRQLCFVVRKVNICYSDGDIWSEWSDKQWEG 333
DB 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEG 327

RESULT 6
US-08-846-340-2
; Sequence 2, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A. 32,724
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-340-2

Query Match 62.3%; Score 1184; DB 4; Length 383;
Best Local Similarity 64.0%; Pred. No. 2e-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPQDPFEIVDPGVLGYLYLQWQPPSLD 60
DB 1 MAFV--HIRCLCFILLCTITGYS-----LEIKVNPQDPFEILDGGLLYLQWQPPVIE 54

QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKTEAKIHTLLPWQCTNGSEVQ 120
DB 55 KFKGCTLEYELKYRNVDSDSWKTIITRNLIYKDGFDLNGKTEGKIRTHLSEHCTNGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPFGIGVLLDTNLYNLFYVVEGLDH 180
DB 115 SPWIEASVIGSDEGSLFKIQDMKCIYNNQYLLCSWKPFGITVSDNTYTFVVEGLDH 174

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFICVNGSSENKPIRSSYFTFOLQNVKPLP 240
DB 175 ALQCADYLQHDKNVCKLSNLDSSDYKDFICVNGSSKLEPIRSSYTFVQLOQNVKPLP 234

QY 241 PVIYLTFTRESCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNE 300
DB 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDKMLKRRANE 294

QY 301 TRQLCFVVRKVNICYSDGDIWSEWSDKQWEG 333
DB 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEG 327

RESULT 7
US-07-757-390-13
; Sequence 13, Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-757-390-13

Query Match 15.5%; Score 294.5; DB 1; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-22;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

Qy 27 DTEKVNPPQDFEIVDPGVLGYLYLQWOPPLSLDHFKECTVEYELKYRNIGSETWTKTIIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
Qy 87 KNLHYKQGFDLNKGIEAKIHTLLPWOCTNGSEVOSSWAETTYWISPOGIPETKVDMDCV 146
Db 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSGTSSVNLTC 135
Qy 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF---WYEGLDHALQCVDYIKAD 191
Db 136 TTTEDNYSRLRSQVSLHCTWLVTGTDAPETQVFLYRYGSWTE-----ECOEYSKDT 189
Qy 192 -GONIGCRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQONIVKPLPPVLTFT 248
Db 190 LGRNIACFPFTFILSKGRDMLAVLVNGSSKHSAIRPPDQLFALHAIDQINPPLNVTAEI 249
Qy 249 ESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLVATVENETVTLKTTNETROLCFVW 308
Db 250 EGT-RLSIQWEKPYSAFPIHCFDYEIVKHNTNRNGVLOIEKLTNAFISIIDLSKYDVQV 308
Qy 309 RAAVSSMCREAGLWSEMS-QPIYVGNDEHK 337

RESULT 8
US-08-442-282-13
Sequence 13, Application US/08442282
Patent No. 5760204
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-442-282-13

Query Match 15.5%; Score 294.5; DB 1; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-22;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

Qy 27 DTEKVNPPQDFEIVDPGVLGYLYLQWOPPLSLDHFKECTVEYELKYRNIGSETWTKTIIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
Qy 87 KNLHYKQGFDLNKGIEAKIHTLLPWOCTNGSEVOSSWAETTYWISPOGIPETKVDMDCV 146
Db 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSGTSSVNLTC 135
Qy 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF---WYEGLDHALQCVDYIKAD 191
Db 136 TTTEDNYSRLRSQVSLHCTWLVTGTDAPETQVFLYRYGSWTE-----ECOEYSKDT 189
Qy 192 -GONIGCRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQONIVKPLPPVLTFT 248
Db 190 LGRNIACFPFTFILSKGRDMLAVLVNGSSKHSAIRPPDQLFALHAIDQINPPLNVTAEI 249
Qy 249 ESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLVATVENETVTLKTTNETROLCFVW 308
Db 250 EGT-RLSIQWEKPYSAFPIHCFDYEIVKHNTNRNGVLOIEKLTNAFISIIDLSKYDVQV 308
Qy 309 RAAVSSMCREAGLWSEMS-QPIYVGNDEHK 337

RESULT 9
US-08-442-281-13
Sequence 13, Application US/08442281
Patent No. 5807991
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,281
FILING DATE:
CLASSIFICATION:

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 16,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-281-13

Query Match 15.5% Score 294.5; DB 1; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-22;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

QY 27 DTEIKVNPQDFEIVDPGLYGLYLQWQPLSLDHFKECTVEYELKYRNIGSETWKTIIIT 86
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 DEKISLLPPVNFITKVGT-LAQVLLQWPNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
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QY 87 KNLHYKGFDLNKGIEAKIHLLPWQCTNGSEVSSWAETTYISPOGIPETKYVQDMDCV 146
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 ES---KCVTILHKGFSAVRIILQ---NDHSLASSWASAEHL-APPGSGTSSVNLCT 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 147 -----YNNQYLL-CSWKKPGIGVLLDTNLYF---WYEGLDHALQCVDYIKAD 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 TWTEDNYSRLRSQVSLHCHWLVGTDAPEDTQFLYIRYGSWTE-----ECOEYSKDT 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 192 -GQNIQGRFP--YLEASDYKDFYICVNGSENKPIRSYFTFQLNIVKPLPPVLTFR 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 LGRNIACWFPRFTILSKGRDLAVLVNGSSKHSALRPDQFLFALHAIQINPPLNVTA 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVTATVENETTYTLKTTNETQLCFV 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 EGT-RLSQWEKPVSAFPIHCFDYEYKIHNRNGYLQIEKLTNAFISIIDLSKYDVQ 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 RSKVNIYCSDDGIWSEWSDKOCWEGEDLSK 338
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337
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RESULT 10
US-08-939-727-13
; Sequence 13 Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 16,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-939-727-13

Query Match 15.5% Score 294.5; DB 2; Length 420;
Best Local Similarity 28.2%; Pred. No. 3.2e-22;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

QY 27 DTEIKVNPQDFEIVDPGLYGLYLQWQPLSLDHFKECTVEYELKYRNIGSETWKTIIIT 86
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 DEKISLLPPVNFITKVGT-LAQVLLQWPNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 87 KNLHYKGFDLNKGIEAKIHLLPWQCTNGSEVSSWAETTYISPOGIPETKYVQDMDCV 146
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 ES---KCVTILHKGFSAVRIILQ---NDHSLASSWASAEHL-APPGSGTSSVNLCT 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 147 -----YNNQYLL-CSWKKPGIGVLLDTNLYF---WYEGLDHALQCVDYIKAD 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 TWTEDNYSRLRSQVSLHCHWLVGTDAPEDTQFLYIRYGSWTE-----ECOEYSKDT 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 192 -GQNIQGRFP--YLEASDYKDFYICVNGSENKPIRSYFTFQLNIVKPLPPVLTFR 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 190 LGRNIACWFPRFTILSKGRDLAVLVNGSSKHSALRPDQFLFALHAIQINPPLNVTA 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVTATVENETTYTLKTTNETQLCFV 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 EGT-RLSQWEKPVSAFPIHCFDYEYKIHNRNGYLQIEKLTNAFISIIDLSKYDVQ 308
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 RSKVNIYCSDDGIWSEWSDKOCWEGEDLSK 338
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-07-757-390-14
; Sequence 14 Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
```



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; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-281-14

```

```

Query Match 15.4%; Score 293.5; DB 1; Length 396;
Best Local Similarity 27.9%; Pred. No. 3.7e-22;
Matches 92; Conservative 58; Mismatches 145; Indels 35; Gaps 13;

```

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QY 27 DPEIKVNPQDFEIVDPGLYLGVLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DEKISLLPPVNFITKVTC-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 87 KNLHYKQDFDLNKGIEAKIHLLPWQCTNGSEVOSSWAETTYTISPQGIPTKVQDMDCV 146
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 ES---KCVTILHKGFSAVRITLQ---NDHSLASSWASAEHL-APPGSPGTSIVNLTCT 135
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYFY---WYEGLDHALQCVDIKAD 191
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TMTEDNYSRLRSYQVSLHCTWLVTGTDAPDTQFLYIRYGSWTE-----ECOYEYSKDT 189
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 192 -GQNGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQNLQIVKPLPPVLTFT 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACWFPRTFILSKGRDMLAVLVNGSSKHSALRPDQLFALHAIDQINPPLNVAEI 249
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIEIREDDTLVATVENETTYTLTKTNETQLCFV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEYVKHNRNGYLQIEKLTNAFTSIIDLSKYDVQV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 309 RSKVNIYCSDDGIWSEWSKOCWEGEDLSK 338
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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```

RESULT 14
US-08-939-727-14
; Sequence 14, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor

```

```

; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennle & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-939-727-14

```

```

Query Match 15.4%; Score 293.5; DB 2; Length 396;
Best Local Similarity 27.9%; Pred. No. 3.7e-22;
Matches 92; Conservative 58; Mismatches 145; Indels 35; Gaps 13;

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QY 27 DTEIKVNPQDFEIVDPGLYLGVLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DEKISLLPPVNFITKVTC-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 87 KNLHYKQDFDLNKGIEAKIHLLPWQCTNGSEVOSSWAETTYTISPQGIPTKVQDMDCV 146
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 ES---KCVTILHKGFSAVRITLQ---NDHSLASSWASAEHL-APPGSPGTSIVNLTCT 135
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYFY---WYEGLDHALQCVDIKAD 191
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TMTEDNYSRLRSYQVSLHCTWLVTGTDAPDTQFLYIRYGSWTE-----ECOYEYSKDT 189
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 192 -GQNGICRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQNLQIVKPLPPVLTFT 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACWFPRTFILSKGRDMLAVLVNGSSKHSALRPDQLFALHAIDQINPPLNVAEI 249
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIEIREDDTLVATVENETTYTLTKTNETQLCFV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEYVKHNRNGYLQIEKLTNAFTSIIDLSKYDVQV 308
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 309 RSKVNIYCSDDGIWSEWSKOCWEGEDLSK 338
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

RESULT 15
US-08-836-561-106
; Sequence 106, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi

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Search completed: September 1, 2001, 19:08:36
Job time: 163 sec

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Query Match      15.4%; Score 293; DB 3; Length 313;
Best Local Similarity 28.3%; Pred. No. 2.9e-22;
Matches 90; Conservative 55; Mismatches 139; Indels 34; Gaps 12;

QY 27 DTEIKVNPDPDEFIVDGYLGYLQWQPPLSLDHFKECTVEYELKYNIGSETWTKIIT 86
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5 DEKISLLPPVNFITKVTG-LAQVLLWQKPNPDQEQ-RNVNLEYQVKINAPKREDDYETRI 62
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 87 KNLHYKDGDFLKNKGIEAKIHTLLPWQCTNGSEVGSSWAETTYTWSPOGIPETKYQDMDCV 146
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 63 ES---KCVTILHKGFSASVRTILQ---NDHSLCLASSWASAEHL-APGSPGTSVVLNLTCT 115
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 147 -----YNNQYLL-CSWKPGIGVLLDTNINLPY-----WYEGLDHALQCVDYIKAD 191
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 116 TTTEDNYSRLRSYQVSLHCTWLVTGTDAPETQFLVYRYGSWTE-----ECQEYSKDT 169
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 192 -GQNIQCRFP--YLEASDYKDFYICVNGSSSENKPIRSYTFQFQINIVKPLPPVYLFPTR 248
   | : | | | | : : : : | : | : | : | : | : | : | : | : | : | : |
Db 170 LGRNIACWFRTFLSKGRDWLAVLVNGSSKHSASIRFPDQLFALHAIQINPPLNVNLTAEI 229
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 249 ESSCEIKLKSIPLGPTPARCFDYEIEIRDDTFLVTAVENETYTLKTTNITQLQCFVV 308
   | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 230 EGT-RLSIQWEKPSAPPIHCFDYEYVKIHNTRNGYLQIEKLTWNAFISIIDLSKYDVQV 288
   | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 309 RSKVNIYCSDDGIGWSEWS 326
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 289 RAAVSSMCREAGLWSEWS 306
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:26 ; Search time 24.79 Seconds
(without alignments)
465.676 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_337

Perfect score: 1873

Sequence: 1 MAFVCLATGCLYFLITTF.....; DDGIWSEWSDKOCWEGEDLS 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1873	100.0	380	1	IL132_HUMAN
2	282.5	15.6	420	1	IL5R_HUMAN
3	289.5	15.5	424	1	IL31_MOUSE
4	285	15.2	427	1	IL131_HUMAN
5	254	13.6	831	1	PLRLR_CHICK
6	229	12.2	415	1	IL5R_MOUSE
7	228	12.2	831	1	PLRLR_MELGA
8	210.5	11.2	830	1	PLRLR_COLLII
9	202.5	10.8	369	1	CYRG_HUMAN
10	199.5	10.7	373	1	CYRG_CANFA
11	198.5	10.6	369	1	CYRG_MOUSE
12	180	9.6	379	1	CYRG_BOVIN
13	179	9.6	878	1	IL3B_MOUSE
14	165	8.8	581	1	PLRLR_BOVIN
15	165	8.8	610	1	PLRLR_RAT
16	160	8.5	897	1	CYRB_HUMAN
17	159	8.5	608	1	PLRLR_MOUSE
18	155.5	8.3	896	1	CYRB_MOUSE
19	151	8.1	622	1	PLRLR_HUMAN
20	150.5	8.0	917	1	IL6B_MOUSE
21	150	8.0	581	1	PLRLR_CEREL
22	147	7.8	616	1	PLRLR_RABIT
23	145.5	7.8	862	1	IL2S_HUMAN
24	133.5	7.1	400	1	GMCR_HUMAN
25	130.5	7.0	378	1	IL3R_HUMAN
26	128	6.8	630	1	PLRLR_ORENI
27	126.5	6.8	874	1	IL2S_MOUSE
28	126.5	6.8	918	1	IL6B_HUMAN
29	123.5	6.6	1097	1	LIER_HUMAN
30	123.5	6.1	1165	1	LEPR_HUMAN
31	112.5	6.0	1630	1	PTPD_DROME
32	109.5	5.8	918	1	IL6B_RAT
33	107	5.7	634	1	GHR_BOVIN

RESULT 1

ID	IL132_HUMAN	STANDARD;	PRT;	380 AA.
AC	Q14627; O00667;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13 BINDING PROTEIN).			
GN	IL13RA2 OR IL13R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Renal cell carcinoma;			
RX	MEDLINE=96279273; PubMed=8663118;			
RA	Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N., Ferrara P.;			
RA	"Cloning and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha chain.";			
RT	J. Biol. Chem. 271:16921-16926(1996).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Testis;			
RC	Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H., Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;			
RA	Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Brain;			
RX	MEDLINE=97321053; PubMed=9177784;			
RA	Guo J., Apiou F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;			
RT	"Chromosome mapping and expression of the human interleukin-13 receptor.";			
RL	Genomics 42:141-145(1997).			
CC	-1- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13 (IL-13), BUT NOT TO IL-4.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X95302; CAA64617.1; -;			
DR	EMBL; U70981; AAB1170.1; -;			
DR	EMBL; Y08768; CAA70021.1; -;			
DR	MM; 300130; -;			

Q28575 ovis aries
P40233 mus musculus
Q99062 homo sapien
P19756 sus scrofa
O62959 rattus norv
P48336 mus musculus
P22063 rattus norv
P26952 mus musculus
P10912 homo sapien
P08169 bos taurus
P70289 mus musculus
P19941 oryctolagus

ALIGNMENTS

```
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
DR Pfam; PF00041; fn3.1;
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT DISULFID 184 197
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B562C887 CRC64;

Query Match 100.0%; Score 1873; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
DB 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60

QY 61 HFKECTVEYELKYRNISETWTKTIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
DB 61 HFKECTVEYELKYRNISETWTKTIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDYNLNFYWEGLDH 180
DB 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDYNLNFYWEGLDH 180

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQIQNIVKPLP 240
DB 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQIQNIVKPLP 240

QY 241 PVYLTFRESSECEIKLWSIPLGPPIPCFDFEIEIRDDDTLTAIVENETYLTKTNE 300
DB 241 PVYLTFRESSECEIKLWSIPLGPPIPCFDFEIEIRDDDTLTAIVENETYLTKTNE 300

QY 301 TROLCFVVRKVNIVCSDDGIWSEMSDKQWGEDLS 337
DB 301 TROLCFVVRKVNIVCSDDGIWSEMSDKQWGEDLS 337

RESULT 2
ID IL5R_HUMAN STANDARD; PRT; 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125 ANTIGEN).
DE IL5RA OR IL5R.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
RN 2
RP SEQUENCE FROM N.A.
RX MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;

RT InterPro; IPR001777; -
RT InterPro; IPR002465; -
RT Pfam; PF00041; fn3.1;
RT PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
RN Receptor; Transmembrane; Glycoprotein; Signal.
RP SIGNAL 1 26
RP CHAIN 27 380
RP DOMAIN 27 343
RP TRANSMEM 344 363
RP DOMAIN 364 380
RP DISULFID 145 155
RP DISULFID 184 197
RP CARBOHYD 115 115
RP CARBOHYD 215 215
RP CARBOHYD 290 290
RP CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B562C887 CRC64;

Query Match 100.0%; Score 1873; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
DB 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60

QY 61 HFKECTVEYELKYRNISETWTKTIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120
DB 61 HFKECTVEYELKYRNISETWTKTIITKNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVQ 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDYNLNFYWEGLDH 180
DB 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDYNLNFYWEGLDH 180

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQIQNIVKPLP 240
DB 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQIQNIVKPLP 240

QY 241 PVYLTFRESSECEIKLWSIPLGPPIPCFDFEIEIRDDDTLTAIVENETYLTKTNE 300
DB 241 PVYLTFRESSECEIKLWSIPLGPPIPCFDFEIEIRDDDTLTAIVENETYLTKTNE 300

QY 301 TROLCFVVRKVNIVCSDDGIWSEMSDKQWGEDLS 337
DB 301 TROLCFVVRKVNIVCSDDGIWSEMSDKQWGEDLS 337

Query Match 15.6%; Score 292.5; DB 1; Length 420;
Best Local Similarity 27.8%; Pred. No. 4.4e-17;
Matches 91; Conservative 58; Mismatches 143; Indels 35; Gaps 13;

QY 27 DTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLDHFKECTVEYELKYRNISETWTKTIIT 86
DB 25 DEKISLLPPVNFYIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAKEDDYETRI 82

QY 87 KNLHYKDGFDLNGKIEAKIHLLPWOCTNGSEVOSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES---KCVTILHKGFSASVRLIQ---NDHSLASSWASAEHLH-APPGSPGTSVNLCT 135

"Molecular basis of the membrane-anchored and two soluble isoforms of the human interleukin 5 receptor alpha subunit";
Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
[3]
SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
MEDLINE=92005669; PubMed=1833065;
Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J., Fiers W., Plaetinck G.;
"A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-specific alpha chain and a beta chain shared with the receptor for GM-CSF";
Cell 66:1175-1184(1991).
-1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN BINDS TO IL-5.
-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY ALTERNATIVE SPLICING
-1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
-1- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw125.htm".
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EMBL; M96652; AAA59152.1; -
EMBL; M96651; AAA59151.1; -
EMBL; M75914; AAA36110.1; -
EMBL; A26249; CAA01793.1; -
EMBL; A24587; CAA01731.1; -
EMBL; A26251; CAA01794.1; -
PIR; A40267; A40267.
MIM; 147851; -
InterPro; IPR000950; -
InterPro; IPR002465; -
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420
FT DOMAIN 21 342
FT TRANSMEM 343 362
FT DOMAIN 363 420
FT CARBOHYD 35 35
FT CARBOHYD 131 131
FT CARBOHYD 216 216
FT CARBOHYD 244 244
FT VARSPPLIC 333 335
FT VARSPPLIC 336 420
FT VARSPPLIC 333 333
FT VARSPPLIC 334 420
SQ SEQUENCE 420 AA; 47700 MW; 420681FBC6B51700 CRC64;
INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
NDE -> FSR (IN SOLUBLE ISOFORM S1).
MISSING (IN SOLUBLE ISOFORM S1).
N-> K (IN SOLUBLE ISOFORM S2).
MISSING (IN SOLUBLE ISOFORM S2).
```

```
QY 147 -----YNNQYLL-CSWKPICIGVLLDTNLYF-----WYEGLDHALQCVDYIKAD 191
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TTTTNDYNSRLRSQVSLHCTWLVTGTDAPEDQYFLYRYGSWTE-----ECQEYSKOT 189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -QONIGCRFP--YLEASDYKDFYICVNGSSNKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACWFPRFTLSLGRDWSLVNGSSKHSARIPDFQALFALHAIDQINPLNVAEI 249
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLWSIPGLPIPARCFDEYIEIREDDTTLVATVENETITLKTNETQLCFV 308
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 EGT-RLSIQWEKPSAPFIHCFDEYVHINRNGYLQIEKLTWNAFISIDDLKSYDVQV 308
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 RSKVNIYCSDDGIWSESDKQCEGED 335
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGN 334
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
ID IL131_MOUSE STANDARD; PRT; 424 AA.
AC O09030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-
DE 13RA-1) (INTERLEUKIN-13 BINDING PROTEIN) (NR4).
GN IL13RA1 OR IL13RA OR IL13R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96133964; PubMed=8552669;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin
RT 13 receptor that is also a component of the interleukin 4 receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY
CC SIMILARITY).
CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDNEY,
CC TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL; S80963; AAB50695.1; -
DR MGD; MGI:105052; IL13ra.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 424 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
FT DOMAIN 26 340 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 341 364 POTENTIAL.
FT DOMAIN 365 424 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 37 100 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 44 93 POTENTIAL.
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FT DISULFID 132 142 BY SIMILARITY.
FT DISULFID 171 183 BY SIMILARITY.
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;

Query Match 15.5%; Score 289.5; DB 1; Length 424;
Best Local Similarity 25.8%; Pred. No. 7.8e-17;
Matches 93; Conservative 63; Mismatches 131; Indels 73; Gaps 17;

QY 8 IGCYLTETLIST-TFGCTSSSDTEIKVNPQQDFEIVDPGYGLYLOQPPPLSLDHFRECT 66
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 LGELLVLLLTATVGVAAA---TEVQPPVTNLSVSVENCTIITWSPPGAS--PNCT 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 VEY-----ELKYNIGSETWKTITITKLNHYKDFDLNKGIEAKIHTLLPWQCT-NGSEVQ 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 LRYFSEHEDDQDKKIAPET-----HRKEELPLDEKICLVGS---QCSANESEKP 108
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 SSWAETTYWIS-POGIPETKVQDMQVYVYNNQYLLCSWKPGIGVLLDTNNTFLTWYEGLD 179
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 109 SPLVKKC--ISPPGDPESAVENTELKCIWHNLSYMKCSWLPGRNTSPDTHLYTYWYSSLE 166
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 HALOCVDYIKADGONIGCRFPYLEAS---DYKDFYICVNGSSNKPIRSYFTFQNLQIV 236
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 167 KSRQC-ENIYREGQHIACSFKLTKEPSEFQNVQIMVKDNAGK--IRPSKIVSLTSYV 223
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 237 KPLPPVLTITRESSCEIKLWSIPGLPIPARCFDEYIEIR----- 277
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 KPDP-PIHKLKLLKNGALLVQKNPN-FRSCLTYEVVNNVTQDRHNILEVEDKCON 281
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 278 -EDDTL-----VTATVENETITLKTNETQLCFVVRKVNKYCSDGIGWSEWSKQ 329
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 282 SESDRNMEGTSFQLPGVLGADAVYTVRVVTKNLCF-----DDNKLWSDWSEAQ 331
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
ID IL131_HUMAN STANDARD; PRT; 427 AA.
AC P78552; Q99656; Q95646;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (IL-13R-ALPHA-1) (IL-
DE 13RA-1).
GN IL13RA1 OR IL13RA OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97165986; PubMed=9013879;
RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,
RA Ferrara P.;
RA "Cloning of the human IL-13R alpha chain and reconstitution with the
RT IL4R alpha of a functional IL-4/IL-13 receptor complex."
RL FEBS Lett. 401:163-166(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
RA Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
RA Eugster H.P., Bonnefoy J.Y.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
```



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FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 830 AA; 94507 MW; 38074E83CDF69EFF CRC64;

Query Match 11.28; Score 210.5; DB 1; Length 830;
Best Local Similarity 24.78; Pred. No. 6.4e-10;
Matches 86; Conservative 47; Mismatches 156; Indels 59; Gaps 14;

QY 18 TFGCTSSDTEIKVNPQDFEIVDPGLG-----DPQVDVTISVQDPAPVNLSTETKTSASTTYLLAKW 150
DB 97 TTYNTVMAMEIGNSS-----DPQVDVTISVQDPAPVNLSTETKTSASTTYLLAKW 150

QY 54 QPPLSLDFKECTV-EYELKYNIGSETWTKIITKNLHYKDFGLNKIGIEAKIHTLLPWQ 112
DB 151 SPPLADVTSSHYRYELRLKPEKEWEIV---SVGVQYQKVNRLQAGVKYVQVR 206

QY 113 CTNGSEVSSWAETTYTISPOG-IPETKVDQMDCCYVYNNQYLLCSWPKGIGVLLDTNYNL 171
DB 207 CVLDIGENSESSRHHIPNGESPPEKPTTIKCRSPKETFTCWKPKSGDGGHPTNTL 266

QY 172 FYWEGDLHALQVDYIKADQNGICRFPYLEADYKDFYICVNGSSSENKPIRSYFTFO 231
DB 267 LYSKEGEERVCEPDY-KTAGPN-SCYFDKKHTSFWTIYNTVKTATNEIGNSVSDPLYVD 324

QY 232 LONIVKPLPPVYLFTRESSCEIK----LKWS-IPLGPAPA-RCFDVEIEIREDDTFLV 284
DB 325 VTYIVQTPPPVNVLELKTNNRPYLVLTWSPPLADVRGWLTLDELRLKPEEA--- 381

QY 285 TATVENETTYLTKTNETRQLCFV-----RSKNVNYCSD--GIWSEWS 326
DB 382 -----EWEETIFVGQTHYKMFSLNPGKKYIVQIHCKPDHGHGSNWS 424

RESULT 9
CYRG_HUMAN
ID CYRG_HUMAN STANDARD; PRT; 369 AA.
AC P31785;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-
DE 2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64) (CD132 ANTIGEN).
GN IL2RG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92335883; PubMed=1631559;
RA Takeshita T., Asao H., Ohkani K., Ishii N., Kumaki S., Tanaka N.,
RA Munakata H., Nakamura M., Sugamura K.;
RT "Cloning of the gamma chain of the human IL-2 receptor.";
RL Science 257:379-382(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93293887; PubMed=8514792;
RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;
RT "Characterization of the human interleukin-2 receptor gamma chain
RT gene.";
RL J. Biol. Chem. 268:13601-13608(1993).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.
```

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RX MEDLINE=94004847; PubMed=8401490;
RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,
RA Willard H., Henthorn P.S.;
RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated
RL in X-linked severe combined immunodeficiency, SCIDX1.";
RN Hum. Mol. Genet. 2:1099-1104(1993).
RP [4]
RX IDENTIFICATION AS A IL-4R SUBUNIT.
RX MEDLINE=94090315; PubMed=8266076;
RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
RA Arai K.-I., Sugamura K.;
RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
RT receptors for IL-2 and IL-4.";
RL Science 262:1874-1877(1993).
RN [5]
RX IDENTIFICATION AS A IL-4R SUBUNIT.
RX MEDLINE=94090317; PubMed=8266078;
RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,
RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
RA Leonard W.J.;
RT "Interleukin-2 receptor gamma chain: a functional component of the
RL interleukin-4 receptor.";
RN Science 262:1880-1883(1993).
RP [6]
RX IDENTIFICATION AS A IL-7R SUBUNIT.
RX MEDLINE=94090316; PubMed=8266077;
RA Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
RA Leonard W.J.;
RT "Interleukin-2 receptor gamma chain: a functional component of the
RL interleukin-7 receptor.";
RN Science 262:1877-1880(1993).
RP [7]
RX 3D-STRUCTURE MODELING OF 57-248.
RX MEDLINE=95111953; PubMed=7529123;
RA Bamorough P., Hedecock C.J., Richards W.G.;
RT "The interleukin-2 and interleukin-4 receptors studied by molecular
RL modelling.";
RN Structure 2:839-851(1994).
RP [8]
RX VARIANTS XSCID PHE-1L15; CYS-240 AND ILE-241.
RX MEDLINE=94130970; PubMed=8299698;
RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
RA de Saint Basile G.;
RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
RL severe combined immunodeficiency disease result in the loss of
RL high-affinity IL-2 receptor binding.";
RN Eur. J. Immunol. 24:475-479(1994).
RP [9]
RX VARIANT XSCID LYS-68.
RX MEDLINE=94375038; PubMed=8088810;
RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
RA de Saint Basile G.;
RT "Detection of three nonsense mutations and one missense mutation in
RL the interleukin-2 receptor gamma chain gene in SCIDX1 that
RL differently affect the mRNA processing.";
RN Genomics 21:291-293(1994).
RP [10]
RX VARIANT XSCID HIS-162.
RX MEDLINE=94300093; PubMed=8027558;
RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
RT "Impairment of ligand binding and growth signaling of mutant IL-2
RL receptor gamma-chains in patients with X-linked severe combined
RL immunodeficiency.";
RN J. Immunol. 153:1310-1317(1994).
RP [11]
RX VARIANT XSCID ASN-39.
RX MEDLINE=95023932; PubMed=7937790;
RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
RA de Saint Basile G.;
RT "Defective human interleukin 2 receptor gamma chain in an atypical X
RL chromosome-linked severe combined immunodeficiency with peripheral T
RL cells.";
```

Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
[12]
RN VARIANTS XSCID CYS-226 AND HIS-226.
RX MEDLINE=93397841; PubMed=7668284;
RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
RT gene causing human X-linked severe combined immunodeficiency.";
RL Am. J. Hum. Genet. 57:564-571(1995).
RN [13]
RN VARIANT XSCID SER-183.
RX MEDLINE=96013903; PubMed=7557965;
RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
RA Levinsky R.L., Kinnon C.;
RT "Screening for mutations causing X-linked severe combined
RT immunodeficiency in the IL-2R gamma chain gene by single-strand
RT conformation polymorphism analysis.";
RL Hum. Genet. 96:427-432(1995).
RN [14]
RN VARIANT XSCID GLN-237 G-H-W INS.
RX MEDLINE=95164726; PubMed=7860773;
RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
RT gamma-chain mutation causing X-linked severe combined
RT immunodeficiency.";
RL J. Clin. Invest. 95:895-899(1995).
RN [15]
RN VARIANT XSCID GLN-271.
RX MEDLINE=95190013; PubMed=7883965;
RA Schmaisteg F.C., Leonard W.J., Noguchi M., Berg M., Rudloff H.E.,
RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
RT "Missense mutation in exon 7 of the common gamma chain gene causes a
RT moderate form of X-linked combined immunodeficiency.";
RL J. Clin. Invest. 95:1169-1173(1995).
RN [16]
RN VARIANT XSCID ARG-115.
RX MEDLINE=97042245; PubMed=8900089;
RA Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B.,
RA Mueller-Fleckenstein I., Horneff G., Schrotten H., Fischer A.,
RA de Saint Basile G.;
RT "Atypical X-linked severe combined immunodeficiency due to possible
RT spontaneous reversion of the genetic defect in T cells.";
RL New Engl. J. Med. 335:1563-1567(1996).
RN [17]
RN VARIANT XSCID GLN-285.
RX MEDLINE=97295088; PubMed=9150740;
RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
RA Cant A., Kinnon C.;
RT "B-cell-negative severe combined immunodeficiency associated with a
RT common gamma chain mutation.";
RL Hum. Genet. 99:677-680(1997).
RN [18]
RN VARIANT XSCID CYS-222.
RX MEDLINE=98064061; PubMed=9399950;
RA Sharfe N., Shahar M., Roifman C.M.;
RT "An interleukin-2 receptor gamma chain mutation with normal thymus
RT morphology.";
RL J. Clin. Invest. 100:3036-3043(1997).
RN [19]
RN FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
RN INTERLEUKINS.
RN PROBABLY ALSO THE IL-13 RECEPTORS.
RN SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
RN IL-13 RECEPTORS.
RN SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
RN DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
RN IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMAGLOBULINEMIA, SWISS TYPE
RN OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
RN SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
RN SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
RN DATABASE: NAME=PROV; NOTE=CD guide CD132 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd132.htm".
RN DATABASE: NAME=IL2RGbase; NOTE=X-linked SCID mutation database;
WWW="http://www.nhgri.nih.gov/DIR/GMBB/XSCID/".
RN [20]
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DR EMBL; D11086; BAA01857.1; -
DR EMBL; L12183; AAA59145.1; -
DR EMBL; L12178; AAA59145.1; JOINED.
DR EMBL; L12176; AAA59145.1; JOINED.
DR EMBL; L12177; AAA59145.1; JOINED.
DR EMBL; L12179; AAA59145.1; JOINED.
DR EMBL; L12180; AAA59145.1; JOINED.
DR EMBL; L12181; AAA59145.1; JOINED.
DR EMBL; L12182; AAA59145.1; JOINED.
DR EMBL; L19546; AAC37524.1; -
DR PIR; A42565; A42565.
DR PDB; 1ILN; 26-JAN-95.
DR PDB; 308380; -
DR MIM; 300400; -
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR InterPro; IPR002465; -
Query Match 10.88; Score 202.5; DB 1; Length 369;
Best Local Similarity 24.88; Pred. No. 1.1e-09;
Matches 61; Conservative 45; Mismatches 111; Indels 29; Gaps 9;
QY 97 LNKIEAKIHTLLPQCTNGSE-VQSSWAETTYWISPGIPETKVDQMDCVYNNQVLLC 155
Db 19 LGVGLNTILT-----PNGNEDTADFFLTMTDSLSVSTLPLPEVQCFVFNVMNC 72
QY 156 SW-----KPGIGVLLDTNLYFYWEGLDH--ALQCVDIYIKADQGNIGCRFPYLEASDY 207
Db 73 TWNSSEPPQP-----TNLTLYWYKNSDNDKVQKSHVLFSEITSGCOLQKKETHLY 125
QY 208 KDFVICYNGSSSEKPIRSSYFTFQLONTVPLPPVYLTFTFTRESSCEIKLKWISPLGPIPA 267
Db 126 QTFVYVQDPRE--PRRQATQMLKQLNLVLPWAPENUTLHLKLSQLELNNW---NRFNL 180
QY 268 RCFDYEIEIREDD-TTLVLTATVE-NETYYTLTKTNETQLCFVVRSKVNIYCSDDGIWSEW 325
Db 181 HCLEHLVQYRTDWDHSWTEQSDVYRHKFSLPSVDGQKRYTFRVRSRNPCLGSGAQHSEW 240
QY 326 SDKQCV 331
Db 241 SHPIHW 246
RESULT 10
CYRG_CANFA
ID CYRG_CANFA STANDARD; PRT; 373 AA.
AC P40321;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=95130114; PubMed=7829104;
RA Henthorn P.S., Somberg R.L., Fimiani V.M., Puck J.M., Patterson D.F.,
RA Felsburg P.J.;
RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
RT severe combined immunodeficiency is a homologue of the human

disease.";
Genomics 23:69-74(1994).
-!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF INTERLEUKINS.
-!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND PROBABLY ALSO THE IL-13 RECEPTORS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED SEVERE COMBINED IMMUNODEFICIENCY.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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EMBL; U04361; AAC48403.1; -;
HSSP; P31785; 11UN.
InterPro; IPR000950; -;
InterPro; IPR001777; -;
InterPro; IPR002465; -;
Pfam; PF00041; fn3; 1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 22 POTENTIAL.
CHAIN 23 373 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
DOMAIN 23 261 EXTRACELLULAR (POTENTIAL).
TRANSMEM 262 283 POTENTIAL.
DOMAIN 284 373 CYTOPLASMIC (POTENTIAL).
DOMAIN 151 249 FIBRONECTIN TYPE-III.
DISULFID 62 72 POTENTIAL.
DISULFID 102 115 POTENTIAL.
CARBOHYD 24 24 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD 249 249 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 373 AA; 42516 MW; 03A0DE1F8B089D8B CRC64;

Query Match 10.7%; Score 199.5; DB 1; Length 373;
Best Local Similarity 26.9%; Pred. No. 2e-09;
Matches 63; Conservative 40; Mismatches 96; Indels 35; Gaps 10;

Qy 115 NGSE-----VQSSWAETTYWISQGIPTKQVDMDCVYNNWOYLCSW-----KPGI 161
Db 31 NGNEDITPDLTATPSET---LSVSLPLEVQ---CFVENVEYMCNTWNSSEPRP-- 82
Qy 162 GVLLDTNNLFVWYGL--DIALQCVDIKADQGNIGCRFPYLEASDYKDFYCVNGSSE 219
Db 83 -----TNLTLYHWYKNSNDKVOEGCHYLFREVAGCWLQKEETHLYETVFVQLDRPE 137
Qy 220 NKPIRSSYFTQLONIKPLPPVLTFTRESSCEKLAWSIPLGPIPARCFDYELIRED 279
Db 138 --PRQSQTKLQNLQNLVWPAPENLTNLNLSQSLLSWS---NRHLDCHLEHVYVQYRSD 192
Qy 280 -DTTLVATVEN-ETVTLKTTNETRQLCFVVRKSKVNIYCSDDGIWSESDKQCW 331
Db 193 WDRSWTEQSDHRNSFSLPSVDGQKFFYFRVRSRNPVLCGSAQRWSESHPIHW 246

RESULT 11
ID CYRG_MOUSE
AC P34902; STANDARD; PRT; 369 AA.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277575; PubMed=8503926;
RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT "Cloning of the mouse interleukin 2 receptor gamma chain:
RT demonstration of functional differences between the mouse and human
RT receptors.";
RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CBA/CA;
RA MEDLINE=93391374; PubMed=8378320;
RA Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
RL IL-2R gamma chain expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93366191; PubMed=8359699;
RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RL gamma.";
RL Gene 130:303-304(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104285; PubMed=7805729;
RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
RA Fischer A., de Saint Basile G.;
RT "The murine interleukin-2 receptor gamma chain gene: organization,
RL chromosomal localization and expression in the adult thymus.";
RL Eur. J. Immunol. 24:3014-3018(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=B6.S;
RA MEDLINE=96341745; PubMed=8750189;
RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
RA Dougherty G.J.;
RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT the adhesion protein CD44.";
RL J. Neurocol. 26:231-239(1995).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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EMBL; D13821; BAA02974.1; -;
EMBL; U21795; AAA64279.1; -;
EMBL; D13565; BAA02760.1; -;
EMBL; L20048; AAA39286.1; -;
EMBL; S75852; AAB32904.1; -;
EMBL; S75844; AAB32904.1; JOINED.
EMBL; S75845; AAB32904.1; JOINED.
EMBL; S75847; AAB32904.1; JOINED.

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DR EMBL; S75848; AAB32904.1; JOINED.
DR EMBL; S75849; AAB32904.1; JOINED.
DR EMBL; S75850; AAB32904.1; JOINED.
DR EMBL; S75851; AAB32904.1; JOINED.
DR EMBL; S75852; AAB32904.1; JOINED.
DR EMBL; S75853; AAB32904.1; JOINED.
DR PIR; JN0592; JN0592.
DR PIR; JN0593; JN0592.
DR HSP; P31785; JN0775.
DR MGD; MGI:96551; IL2Fg.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 369
FT DOMAIN 23 369
FT TRANSMEM 23 369
FT DOMAIN 264 369
FT DOMAIN 285 369
FT DOMAIN 151 250
FT DISULFID 62 72
FT DISULFID 102 115
FT CARBOHYD 71 71
FT CARBOHYD 75 75
FT CARBOHYD 84 84
FT CARBOHYD 96 96
FT CARBOHYD 159 159
FT CARBOHYD 164 164
SQ SEQUENCE 369 AA; 42241 MW; CB2D5AB459077AC7 CRC64;

Query Match 10.6%; Score 198.5; DB 1; Length 369;
Best Local Similarity 26.5%; Pred. No. 2.4e-09;
Matches 54; Conservative 38; Mismatches 95; Indels 17; Gaps 7;

QY 136 PETKYQDMDCVYNNQYLLCSW----KPGIGVLLDTNLYFWYEGDLHAL--QCVDYIK 189
Db 53 PTLPLPEQVCFENIEYNNCTWNSSEPQA-----TNLTLYRYKVSNNFTQECSHYLF 107
QY 190 ADQGNIGCRFPYLEADYKDFYICVNGSSSEKPIRSSYFTFQLONIYKPLPPVYLT 249
Db 108 SKEITSGCQIQKEDQLYQTFVQVL--QDPQKPRRAVQKLNQNLVTPRAPENLTLSNL 165
QY 250 SSECIKLWSPILGPAPARCFDYEIEIRD--DTTLVTATVENE--TYTLTKTTNETRQLCFV 307
Db 166 SESQLELRK--SRHKEKRCQLYLVQYRSNDRSRTWELIVNHEPRSLPSVDELKRYTR 223
QY 308 VRSKYNIIYCSDDGIWSESDKQCV 331
Db 224 VRSRYNPICGSSQQKWSQPVHW 247

RESULT 12
CYRG_BOVIN
ID CYRG_BOVIN STANDARD; PRT; 379 AA.
AC Q95118;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96268473; PubMed=8672241;
RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
```

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gamma gene."
DNA Cell Biol. 15:453-459(1996).
-!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
INTERLEUKINS.
-!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
PROBABLY ALSO THE IL-13 RECEPTORS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; U33748; AAB07812.1; -.
HSP; P31785; IILN.
InterPro; IPR000950; -.
InterPro; IPR001777; -.
InterPro; IPR002465; -.
Pfam; PF00041; fn3; 1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 379
FT DOMAIN 23 269
FT TRANSMEM 270 290
FT DOMAIN 291 379
FT DOMAIN 158 256
FT DISULFID 68 78
FT DISULFID 109 122
FT CARBOHYD 77 77
FT CARBOHYD 81 81
FT CARBOHYD 90 90
FT CARBOHYD 166 166
FT CARBOHYD 171 171
SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 9.6%; Score 180; DB 1; Length 379;
Best Local Similarity 26.0%; Pred. No. 8.5e-08;
Matches 54; Conservative 38; Mismatches 90; Indels 26; Gaps 8;

QY 135 IPEYKQDMDCVYNNQYLLCSW----KPGIGVLLDTNLYFWY---EGLDHALQCV 185
Db 61 LPLPKVQ---CFVFNVEYMNCTWNSSEPQP-----NNLTLYGYRNFGDDKLOECG 110
QY 186 DYKADGNIGCRFPYLEADYKDFYICVNGSSSEKPIRSSYFTFQLONIYKPLPPVYLT 245
Db 111 HYLSEGITSGCWFQKKEIRLYETFFVQLOQDPREHR--KQPKMLKQDLVWPAPENLT 168
QY 246 FTRESSEIKLKWSPILGPAPARCFDYEIEIRD--DTTLVTATVENE--TYTLTKTTNETRQ 303
Db 169 LRNLSEFQLELSWS---NRYLDHCLHLYVQYRSNDRSRTWELIVNHEPRSLPSVDAQKL 225
QY 304 LCFVVRSKVNIYCSDDGIWSESDKQCV 331
Db 226 YTFVRVSRYPNLCGSAQHWSDWSYPIHW 253

RESULT 13
IL3B_MOUSE
ID IL3B_MOUSE STANDARD; PRT; 878 AA.
AC P26954;
DT 01-OCT-1993 (Rel. 27, Created)
DE 01-OCT-1993 (Rel. 27, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR CLASS II BETA CHAIN PRECURSOR (COLONY
DE STIMULATING FACTOR 2 RECEPTOR, BETA 2 CHAIN).
GN CSF2RB2 OR A12CA OR IL3RB2 OR IL3R.
```


Qy 246 F-----TRESSCEIKLWSIP-LGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE 300
Db 130 LEVQLKDKTYLWVWSPPTITDVKTGFTMEYER-----LKPEAEWEIHFTH 182
Qy 301 TRQL-----CFVRSKVNICYSDDGWSEWSDKOCWE 332
Db 183 QTQFKVFDLYPGQKYLQTRCK---PDHGYSRWSQESSVE 220

Search completed: September 1, 2001, 19:16:27
Job time: 509 sec

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PS Claim 1; Figure 2a; 83pp; French.

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R beta
 CC and alpha which can be used as IL-13 antagonists, specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for gene
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immunoassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).

XX Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYFLISTTFTGCTSSDTEIKVNPQQDFEIVDPGVLGYLYLQWQPPLSLD 60
 DB 1 mafvclaigcllyflisttftgctssdteikvnpqdfeidvdpvglylylqwqpplsl 60

QY 61 HFKECTVEYELKYRNIGSETWKTITKNLHYKDGFDLNGKEAKIHLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynigsetwktitknlhykdgfdlنگkeakihllpwqctngsevg 120

QY 121 SSWAETTYWISPOGIPETKVDMDCVYNNQYLLCSKPGIGVLLDYNLFWYEGLDH 180
 DB 121 sswaettywispgipetkvdmdcvynnwqyllcswkpgigvllldnynlfwyegldh 180

QY 181 ALQCVDIKADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
 DB 181 alqcvdikadgqngicrfpyleasdykdfyicvngssenkprrsyftfolqnvkplp 240

QY 241 PVIYLTFTRESCEIKLWSIPGLPIPARCFDYEIREDDTTLVTAVENETYTLKTTNE 300
 DB 241 pviyftfresceiklwsipglpmparcfdyeirreddttlvtatvenetytlkttne 300

QY 301 TROLCFVVRKVNLYCSDGGLWSWSKQCEGEDLS 337
 DB 301 trqlcfvvrskvnlycsddglwswskqcegedls 337

RESULT 2

ID AAW35295 standard; Protein; 380 AA.

XX AAW35295;

XX 27-MAR-1998 (first entry)

XX Human IL-13 binding chain of the IL-13 receptor.

XX Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT /label= signal_sequence
 FT /note= "putative"
 FT 26..380
 FT /label= mature_protein
 FT 26..341
 FT /label= extracellular_domain
 FT 342..362
 FT /label= transmembrane_domain
 FT 363..380
 FT /label= intracellular_domain

XX WO9731946-A1.

PN 04-SEP-1997.

XX 28-FEB-1997; 97WO-US03124.

PR 01-MAR-1996; 96US-0609572.

PA (GEMY) GENETICS INST INC.

PI Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;

XX WPI; 1997-448632/41.

DR N-PSDB; AAT95214.

XX New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transformed cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis

XX Claim 11; Pages 34-35; 49pp; English.

XX The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied,
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.

XX Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYFLISTTFTGCTSSDTEIKVNPQQDFEIVDPGVLGYLYLQWQPPLSLD 60

DB 1 mafvclaigcllyflisttftgctssdteikvnpqdfeidvdpvglylylqwqpplsl 60

QY 61 HFKECTVEYELKYRNIGSETWKTITKNLHYKDGFDLNGKEAKIHLLPWQCTNGSEVQ 120

DB 61 hfkectveyelkynigsetwktitknlhykdgfdlنگkeakihllpwqctngsevg 120

QY 121 SSWAETTYWISPOGIPETKVDMDCVYNNQYLLCSKPGIGVLLDYNLFWYEGLDH 180

DB 121 sswaettywispgipetkvdmdcvynnwqyllcswkpgigvllldnynlfwyegldh 180

QY 181 ALQCVDIKADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240

DB 181 alqcvdikadgqngicrfpyleasdykdfyicvngssenkprrsyftfolqnvkplp 240

QY 241 PVLFTRESSCEIKLWSIPGIPARCFDYIEIREDDTTLVATVENETYLTKTNE 300
Db 241 pvlftressceiklwsipgiparcfdyieireddttlvatvenetytlktne 300
QY 301 TROLCFVVRKSNVYCSDDGIWSEWSKQCEGEDLS 337
Db 301 trqlcfvvrksnvlycsddgiwsewsdkqcegedls 337

RESULT 3
AAW36613
ID AAW36613 standard; Protein; 380 AA.
XX
AC AAW36613;
XX
DT 30-MAR-1998 (first entry)
XX
DE Human Zcytor2 cytokine receptor protein.
XX
KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 340..363
FT FT /label= transmembrane_domain
FT FT 364..380
FT FT /label= intracellular_domain
FT FT 25..339
FT FT /label= ligand_binding_domain
XX
PN WO9733913-A1.
XX
PD 18-SEP-1997.
XX
PF 12-MAR-1997; 97WO-US04043.
XX
PR 13-MAR-1996; 96US-0013345.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
PI O'Hara PJ;
XX
DR WPI; 1997-470820/43.
DR N-PSDB; AAT96782.
XX
PT New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
XX
PS Claim 2; Page 47-48; 79pp; English.

This sequence represents a novel ligand-binding receptor, Zcytor2, which shares homology with cytokine receptors and was isolated from human placental polyA+ RNA. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor, and therapeutically as antagonist.

Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 18; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.6e-176;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLISTFGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
Db 1 mafvclaigclytflistfgctssdteikvnpqdfelvdpvglylqwgppslsld 60
QY 61 HFKECTVEYELKYRNIGSETWKTITTKNLHYKDGFDLANKIEAKITHTLLPQCTNGSEVO 120
Db 61 hfkectveyelkyrnigsetwktitknlhykdgfdlnkgeakhtltpwqctngsevg 120
QY 121 SSWAETTYWISPOGIPETKVDMDCVYNNWQYLLCSWRPGIGVLDTNINFYWYEGLDH 180
Db 121 sswaettywispgipetkvdmdcvynnwqyllcswrpgigvldtyninlfwyegldh 180
QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYTFQLOINVKPLP 240
Db 181 alqcvdyikadqngicrfpyleasdykdfyicvngssenkprrsytfqlnivkplp 240
QY 241 PVLFTRESSCEIKLWSIPGIPARCFDYIEIREDDTTLVATVENETYLTKTNE 300
Db 241 pvlftressceiklwsipgiparcfdyieireddttlvatvenetytlktne 300
QY 301 TROLCFVVRKSNVYCSDDGIWSEWSKQCEGEDLS 337
Db 301 trqlcfvvrksnvlycsddgiwsewsdkqcegedls 337

RESULT 4
AAW41520
ID AAW41520 standard; Protein; 380 AA.
XX
AC AAW41520;
XX
DT 22-JUN-1998 (first entry)
XX
DE Human HR-1 receptor.
XX
KW HR-1 receptor; human; cytokine; infection; asthma; allergy;
KW haematopoietic disorder; tumour; therapy; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT FT /label= Sig_peptide
FT FT 22..380
FT FT /label= Mat_protein
XX
PN WO9747741-A1.
XX
PD 18-DEC-1997.
XX
PF 12-JUN-1996; 96WO-US10262.
XX
PR 12-JUN-1996; 96WO-US10262.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Appelbaum ER, Hu J;
XX
DR WPI; 1998-052308/05.
DR N-PSDB; AAW04131.
XX
PT Nucleic acid sequence encoding human cytokine peptide hormone
PT receptor - useful to treat, prevent or diagnose, e.g. lowered
PT resistance to infection, asthma, allergy or haematopoietic disease
XX
PS Claim 13; Page 62-64; 76pp; English.

CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated the HR-1 receptor, that shows 27% identity
 CC and 52% similarity to the interleukin-5 receptor. Its amino acid
 CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
 CC human testis library. Recombinant HR-1 receptor can be expressed
 CC in claimed host cells, and used in a claimed method for identifying
 CC compounds which bind to, and activate or inhibit, it. HR-1
 CC receptor activators and agonists can be used to treat, prevent or
 CC diagnose predisposition to lowered resistance to infection, asthma,
 CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
 CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer.
 CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
 CC be used to treat conditions associated with HR-1 receptor
 CC overexpression. The antibodies can also be used to determine HR-1
 CC receptor levels, since overexpression may be diagnostic of tumours.
 XX Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTGCTSSDTEIKVNPDPQFEIVDPGVLGYLYLQWQPPPLSLD 60
 DB 1 mafvclaigcltytlftstgctssdteikvnpdpqfeivdpgylgylylqwpplsl 60

QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynigsetwktititknhykdgfdlnkgeakihllpwqctngse 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGLVLDNTNLYFYWVEGLDH 180
 DB 121 sswaettywispgipetkvqdmcdvynnwqyllcswkpglgvldntnlyfywvegl 180

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNIVKPLP 240
 DB 181 alqcvdyikadqngicrfyleasdykdfyicvngsssenkpirssyftfqlqnvkpl 240

QY 241 PVYLTFRESSECEIKLWSPGLPPIPCARCFDYEIEIRDDDTLVTATVENETYTLTKTNE 300
 DB 241 pvytlftressceiklwsiplpkiparcfdyeiieirdddtlvtatvenetytlktne 300

QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQCEGEDLS 337
 DB 301 trqlcfvvrskvnicysdgdiwsewsdkqcegedls 337

RESULT 5
 ID AAW41502
 XX AAW41502 standard; Protein; 380 AA.
 AC AAW41502;
 XX 08-JUN-1998 (first entry)
 DT Human cytokine/peptide receptor, HR-1 receptor.
 DE
 XX
 KW HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
 KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
 KW neutropenia; therapy.
 XX
 OS Homo sapiens.
 XX
 EH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Sig_peptide
 FT 22..380
 FT Protein /label= Mat_protein
 FT /note= "Claim 14"
 XX
 PN EP812913-A2.
 XX

PD 17-DEC-1997.
 XX
 PF 04-JUN-1997; 97EP-0303815.
 XX
 XX 12-JUN-1996; 96US-0017843.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Appelbaum ER, Hu J;
 XX
 XX WPI; 1998-034974/04.
 DR N-PSDB; AAV04075.
 XX
 PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
 PT increase resistance to infections in individuals with trauma and/or
 PT burns
 XX
 XX
 PS Claim 13; Page 27-28; 34pp; English.
 CC
 CC This protein comprises a novel human cytokine/peptide hormone
 CC receptor, designated HR-1 receptor. The amino acid sequence
 CC was deduced from a cDNA clone (see AAV04075) isolated from a human
 CC testis cDNA library. It shows 27% amino acid identity and 52%
 CC similarity with the human interleukin-5 receptor. Also claimed are
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an
 CC agonist to the polypeptide, antibody against the polypeptide, an
 CC antagonist that inhibits the activity of the polypeptide, a process
 CC for diagnosing a disease, or a susceptibility to disease, related
 CC to expression of HR-1 receptor, and a method for identifying
 CC compounds that activate or inhibit the HR-1 receptor. HR-1
 CC receptor protein and polynucleotides can be used for research,
 CC biological, diagnosis and (gene) therapy applications, e.g. to
 CC increase resistance to infections in individuals with trauma and/or
 CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
 CC predisposition to asthma, allergic disorders or disorders of
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
 CC cyclic neutropenia or as a consequence of cytotoxic therapy of
 CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTGCTSSDTEIKVNPDPQFEIVDPGVLGYLYLQWQPPPLSLD 60
 DB 1 mafvclaigcltytlftstgctssdteikvnpdpqfeivdpgylgylylqwpplsl 60

QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkynigsetwktititknhykdgfdlnkgeakihllpwqctngse 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGLVLDNTNLYFYWVEGLDH 180
 DB 121 sswaettywispgipetkvqdmcdvynnwqyllcswkpglgvldntnlyfywvegl 180

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNIVKPLP 240
 DB 181 alqcvdyikadqngicrfyleasdykdfyicvngsssenkpirssyftfqlqnvkpl 240

QY 241 PVYLTFRESSECEIKLWSPGLPPIPCARCFDYEIEIRDDDTLVTATVENETYTLTKTNE 300
 DB 241 pvytlftressceiklwsiplpkiparcfdyeiieirdddtlvtatvenetytlktne 300

QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQCEGEDLS 337
 DB 301 trqlcfvvrskvnicysdgdiwsewsdkqcegedls 337

RESULT 6

AAW33603
ID AAW33603 standard; Protein; 380 AA.

XX
AC AAW33603;

XX
DT 08-JUN-1998 (first entry)

XX
DE Homo sapiens HR-1 receptor.

XX
KW Cytokine; hormone receptor; AIDS; acquired immune deficiency;
KW syndrome; aplastic anaemia; neutropaenia; cancer treatment;
KW infection resistance; diagnosis; tumours; HR-1 receptor;
KW asthma; allergic; haematopoietic; disorder.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"

XX
PN W09747742-A1.

XX
PD 18-DEC-1997.

XX
PF 09-JUL-1996; 96WO-US11459.

XX
PR 12-JUN-1996; 96WO-US10262.

XX
PR 12-JUN-1996; 96US-0017843.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
PI Appelbaum ER, Hu J;

XX
DR WPI; 1998-052309/05.

XX
DR N-PSDB; AAV02295.

XX
PT DNA encoding human cytokine-peptide hormone receptor - useful for
PT treating preventing or diagnosing, e.g. lowered resistance to
PT infection, asthma, allergy, or haematopoietic disease

XX
PS Claim 15; Fig 1; 75pp; English.

XX
CC The sequence is that of the human cytokine/peptide hormone receptor
CC (HR-1 receptor). This, or it's activators or agonists, can be used to
CC treat, prevent or diagnose predisposition to lowered resistance to
CC infection, asthma, allergic or haematopoietic disorders, e.g. where
CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
CC neutropaenia or cytotoxic treatments for cancer. Antagonists of the
CC receptor, e.g. antibodies or fragments of it may be used to treat
CC conditions associated with overexpression of the HR-1 receptor, e.g.
CC those listed above. Antibodies may also be used to assay levels of HR-1
CC receptor, overexpression of which may be diagnostic of tumours, by usual
CC immunoassays; to isolate and identify HR-1 receptor-expressing cells; or
CC for affinity purification of the HR-1 receptor.

XX
SQ Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.6e-176;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLITFTGCTSSSTEIKVNPQPQFEIVDPGLGLYLQWPPPLSLD 60

DB 1 mafvclaigclyltltftgtctssstetkvnppqdfvdpqglgylglwppplsl 60

QY 61 HFKECTVEYELKYNIGSETWKTITITNLYKDGFDLNKNGTEAKHTLLPQCTNGSEVQ 120

DB 61 hfkectveyelkynigsetwktititnlykdgfdlnkngteakhtllpwqctngse 120

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
|||||

DB 121 sswaettywispgipetkvqdmcdvynnwqyllicswkpgigvlltdnynlfywegldh 180
QY 181 ALCQVDYIKADGQNGICRFPPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNVKPLP 240
|||||
DB 181 alqcvdyikadgqngicrfppyleasdykdfyicvngssenkpirssyftfqlqnvkplp 240
|||||
QY 241 PVIYLTFTRESSCEIKLKWSPGLPIPARCFDYEIEIREDDTTLVTATVENEYTLTKTNE 300
|||||
DB 241 pviyftressceiklkwspglpkiparcfdyeieireddttltvtatvenetytlktne 300
|||||
QY 301 TRQICFVVRKVNKYCSDGDIWSEWSKQWEGEDLS 337
|||||
DB 301 trqicfvvrskvniycsddgiwsewskqcgwedls 337
|||||

RESULT 7

AA95296

ID AAY95296 standard; Protein; 380 AA.

XX
AC AAY95296;

XX
DT 12-SEP-2000 (first entry)

XX
DE IL-13 binding chain of human IL-13 receptor.

XX
KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; antiallergic;
KW antiinflammatory; antiasthmatic; vaccine.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /note= "signal peptide"

FT Protein 26..380
FT /note= "mature protein"

FT Domain 26..341
FT /note= "extracellular domain; a polypeptide

FT comprising amino acids 22-334 is
FT specifically claimed in Claim 11(e)"
FT Domain 342..362
FT /note= "transmembrane domain"

FT Domain 363..380
FT /note= "intracellular domain; a polypeptide
FT comprising amino acids 257-383 is
FT specifically claimed in Claim 11(f)"

XX
PN W0200036103-A1.

XX
PD 22-JUN-2000.

XX
PF 13-DEC-1999; 99WO-US29493.

XX
PR 14-DEC-1998; 98US-0211335.

XX
PX (GEMY) GENETICS INST INC.

PA (UYJO) UNIV JOHNS HOPKINS.

XX
PI Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
PI Wills-Karp M;

XX
DR WPI; 2000-431587/37.

XX
DR N-PSDB; AAA27912.

XX
PT New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
PT an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
PT asthma, Grave's disease and inflammatory conditions of the lung -
XX Claim 11(d); Page 53-54; 60pp; English.

XX
CC The present sequence is that of the interleukin-13 binding chain

CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated
 CC human testis cDNA clone (see AAA27912). IL-13bc is a member of
 CC the haematopoietin receptor family that acts as a mediator of
 CC IL-13. The invention provides methods for the recombinant
 CC production of IL-13bc polypeptides, including claimed full-length
 CC IL-13bc, its extracellular domain, and its intracellular domain.
 CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
 CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
 CC of IL-13 and its receptor) can be used to treat conditions in
 CC which IL-13 is implicated, particularly IgE-mediated conditions and
 CC diseases including atopy, allergy, asthma, immune complex diseases
 CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
 CC thyroiditis and Grave's disease), lung inflammation,
 CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
 CC activation, IL-13bc proteins can also be used to enhance macrophage
 CC activation, e.g. in vaccination, treatment of mycobacterial or
 CC intracellular organisms or parasite infections. IL-13bc proteins
 CC may also be used to potentiate the effects of IL-13 in vitro and
 CC in vivo, as diagnostic agents, and to screen for agents capable of
 CC binding to IL-13bc or IL-13 receptor, or which interfere with the
 CC binding of IL-13 to its receptor.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 21; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLFTTFCGTSSTDEIKVNPQDFEIVDPGVLYLQWQPPPLSLD 60
 Db 1 mafvclaigcltytlfttfgctssstdeikvnpqdfvdpvglylylqwppplsl 60

Qy 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLANKGIEAKHTLLPQCNGSEVQ 120
 Db 61 hfkectveyelkynrigsetwktitknlhykdgfdlnkgieakhtllpwqctngse 120

Qy 121 SSWAETTWISPOGIPERKVDMDCVYVNWQVLLCSWPKPGIGVLDITNLYFYWYEGDLH 180
 Db 121 sswaettwisppgipetkvdmdcvyynwqyllcswpkpgigvlditnlyfywye 180

Qy 181 ALQCVDYIKAGQNTGCRPPYLEASDYKDFYICVNGSENKPIRSSYTFOLQNIKPLP 240
 Db 181 alqcvdyikadqngicrfyleasdykdfyicvngsenkpirssytfqlqnikplp 240

Qy 241 PVLFTFRESSCEIKLWSIPLGPAPRCFDEYIEIREDDTLVTATVENETYTLKTNE 300
 Db 241 pvlftfressceiklwsiplgpaprcfdeyieireddtlvtatvenetytlktne 300

Qy 301 TRQLCFVVRKSNVNYCSDDGWSEWSRQCWGEDLS 337
 Db 301 trqlcfvvrksnvnycsddgiwsewsdkqcwgedls 337

RESULT 8
 AAY72136
 ID AAY72136 standard; Protein; 380 AA.
 XX
 AC AAY72136;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
 XX
 KW Human; IL-13; interleukin-13 binding chain of IL-13 receptor; IL13bc;
 KW therapy; tissue fibrosis; Schistosoma infection; surgical incision;
 KW cytosatic; wound; IL-13 related condition; allergic condition;
 KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;
 KW macrophage activation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

Peptide 1..25
 /label= Signal_peptide
 FT Region 1..81
 /note= "This region is identical to the translated
 FT sequence of an expressed sequence tag (EST) identified
 FT as yg99f10.r1 human cDNA clone 41648 5"
 FT Protein 26..380
 /label= Mature_human_interleukin (IL)-13_binding_chain_
 FT of_IL-13_receptor
 FT Domain 26..341
 /note= "Extracellular domain; this region is specifically
 FT claimed in claims 1e, 6e, 15e and 23e"
 FT Domain 342..362
 /note= "Transmembrane domain"
 FT Domain 363..380
 /note= "Intracellular domain; this region is specifically
 FT claimed in claims 1f, 6f, 15f and 23f"
 XX
 PN WO200078336-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-US17103.
 XX
 PR 21-JUN-1999; 99US-0334512.
 XX
 PA (GEMY) GENETICS INST INC.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 PI Wills-Karp M;
 XX
 XX WPI: -2001-080753/09.
 DR N-PSDB: AAD02335.
 XX
 PT Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
 PT in a mammalian subject, involves administering a pharmaceutical
 PT composition comprising IL-13 antagonist -
 XX
 PS Claim 1a; Page 69-70; 72pp; English.
 XX
 CC The invention relates to a method of treating, or inhibiting
 CC the formation of tissue fibrosis in mammals, which involves
 CC administering a pharmaceutical composition comprising interleukin
 CC (IL)-13 antagonist. The protein of the invention is useful for
 CC treating tissue fibrosis resulting from infection with Schistosoma
 CC or from healing of a wound which is a surgical incision, or
 CC inhibiting formation of tissue fibrosis which affects tissues such
 CC as liver, skin epidermis and endodermis, muscle, tendon, cartilage,
 CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
 CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,
 CC biliary tract and gut. It is also used in the treatment or modulation
 CC of various IL-13 related conditions such as allergic conditions,
 CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.
 CC The present sequence is human interleukin (IL)-13
 CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used
 CC to potentiate the effects of IL-13. This protein is also used to
 CC enhance macrophage activation and hence can be used in vaccination
 CC or treatment of mycobacterial or parasitic infections.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 1873; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.6e-176;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLFTTFCGTSSTDEIKVNPQDFEIVDPGVLYLQWQPPPLSLD 60
 Db 1 mafvclaigcltytlfttfgctssstdeikvnpqdfvdpvglylylqwppplsl 60

Qy 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLANKGIEAKHTLLPQCNGSEVQ 120
 Db 61 hfkectveyelkynrigsetwktitknlhykdgfdlnkgieakhtllpwqctngse 120

Db 61 hflectveyelkynrigsetwktiitknlhkydgdldnkgieakihltlpwqctngsevg 120
Qy 121 SSWAETTYWISPOGIPETKVOQMDVCYYNWOYLLCSWKPGLVLLDTNYNLFYWEGLDH 180
Db 121 sswaettywispqgipetkvdqmdcvynwqyilcswkpggvlldtnynlfywegldh 180
Qy 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadqngicrfpyleasdykdfyicvngsssenkpirssyftfqlqnvkplp 240
Qy 241 PVLFTFTRESSCEIKLWSIPLGPPIPARCFDYEIREDDTLTVATVENETYTLTKTNE 300
Db 241 pvlftftressceiklwsiplgpiparcfdyeieireddttltvtatvenetytlktne 300
Qy 301 TRQLCFVVRKVNICYSDGDIWSEWSKQCEGEDLS 337
Db 301 trqlcfvvrskvnicycsddgiwsewsdkqcegedls 337
RESULT 9
ID AAB29748 standard; Protein; 380 AA.
XX
AC AAB29748;
XX
XX 23-FEB-2001 (first entry)
XX
DE Human IL-13 receptor IL-13 binding chain (IL-13bc).
XX
KW Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulneryary;
KW wound healing; schistosoma infection; liver; skin; muscle;
KW cartilage; cardiac tissue; lung tissue; uterine tissue;
KW intestinal tissue; vascular tissue; neural tissue.
XX
OS Homo sapiens.
XX
PN WO200064944-A1.
XX
XX 02-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11612.
XX
XX 28-APR-1999; 99US-0301808.
XX
XX (GEMY) GENETICS INST INC.
XX
XX Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;
XX Whitters MJ, Wood C;
XX
XX WPI; 2001-024676/03.
XX N-PSDB; AAC81416.
XX
XX Treating or inhibiting tissue fibrosis resulting from infection with
XX schistosoma and wound healing involves administering interleukin-13 or
XX interleukin-4 antagonist -
XX
XX Claim 1; Page 76-77; 82pp; English.
XX
XX The invention relates to a method of treating fibrosis in a mammal
XX by administering an interleukin-13 (IL-13) antagonist or an IL-4
XX antagonist. In particular, the IL-13 antagonist is the IL-13 binding
XX chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or
XX soluble fragments thereof. The method is useful for treating or
XX inhibiting the formation of tissue fibrosis resulting from the healing
XX of a wound, including a surgical incision wound, or from infection with
XX schistosoma. The method may be used to treat fibrosis in a variety of
XX tissues, particularly liver tissue, but also skin epidermis, skin
XX endoderms, muscle, tendon, cartilage, cardiac tissue, pancreatic
XX tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,
XX adrenal gland, artery, vein, colon, small intestine, biliary tract or gut
XX tissue. The present sequence represents human IL-13bc.

SQ Sequence 380 AA;
Query Match 100.0%; Score 1873; DB 22; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.6e-176;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFVCLAIGCLYTLFTFGCTSSSDTEIKVNPQDFEIVDPDGYLVLYLQWQPPLSLD 60
Db 1 mafvclaigclytlftsttctssdteikvnpqdfeiwdpdylylylqwpplslid 60
Qy 61 HFKECTVEYELKYRNISETWKTITKLNHLYKDGFDLKNKGIEAKIHITLLPWQCTNGSEVQ 120
Db 61 hflectveyelkynrigsetwktiitknlhkydgdldnkgieakihltlpwqctngsevg 120
Qy 121 SSWAETTYWISPOGIPETKVOQMDVCYYNWOYLLCSWKPGLVLLDTNYNLFYWEGLDH 180
Db 121 sswaettywispqgipetkvdqmdcvynwqyilcswkpggvlldtnynlfywegldh 180
Qy 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadqngicrfpyleasdykdfyicvngsssenkpirssyftfqlqnvkplp 240
Qy 241 PVLFTFTRESSCEIKLWSIPLGPPIPARCFDYEIREDDTLTVATVENETYTLTKTNE 300
Db 241 pvlftftressceiklwsiplgpiparcfdyeieireddttltvtatvenetytlktne 300
Qy 301 TRQLCFVVRKVNICYSDGDIWSEWSKQCEGEDLS 337
Db 301 trqlcfvvrskvnicycsddgiwsewsdkqcegedls 337
RESULT 10
ID AAW36614 standard; Protein; 380 AA.
XX
AC AAW36614;
XX
XX 30-MAR-1998 (first entry)
XX
XX Human Zcytor2 cytokine receptor protein.
XX
XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
XX infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX
XX Homo sapiens.
XX
XX WO9733913-A1.
XX
XX 18-SEP-1997.
XX
XX 12-MAR-1997; 97WO-US04043.
XX
XX 13-MAR-1996; 96US-0013345.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
XX O'Hara PJ;
XX
XX WPI; 1997-470820/43.
XX N-PSDB; AAT96783.
XX
XX New nucleic acid encoding testis-specific cytokine receptor - useful
XX for identification of ligands or antagonists, potentially for use as
XX male contraceptives or for infertility treatment
XX
XX Claim 1; Page 51-53; 79pp; English.
XX
XX This sequence represents a novel ligand-binding receptor, Zcytor2, which
XX shares homology with cytokine receptors and was isolated from a human
XX testis cDNA library. The resulting polypeptide is a receptor for
XX cytokines (particularly interleukin-13) and is expressed on the surface

CC of testicular cells, probably being involved in spermatogenesis. It can
CC be used to detect ligands that promote proliferation and/or
CC differentiation of such cells in cultures and may also be used to treat
CC infertility. Antagonists of this receptor may be used to characterise
CC ligand-receptor interactions and as male-specific contraceptives. By
CC blocking the action of IL-13, receptor antagonists and ligand-binding
CC this receptor can also be used to modulate immune function, e.g. in
CC allergy and asthma, as a diagnostic to determine circulating levels of
CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.
XX
SQ Sequence 380 AA;

Query Match 98.6%; Score 1847; DB 18; Length 380;
Best Local Similarity 99.1%; Pred. No. 2.4e-173;
Matches 334; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFLISTFGCTSSDTEIKVNPDPDFEIVDPGVLGYLQWOPPLSLD 60
DB 1 mafvclaigcltytlflistfgctssdteikvnpdpdfivdpgylylqwgppslid 60
QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNGKIEAKIHTLLPQCTNGSEVQ 120
DB 61 hfkeytveyelkynigsetwktitknlhykdgfdlnkgeakihltllpwqctngsevg 120
QY 121 SSWAETTWISPOGIPETKVDQMCVYVNWQYLLCSWPKGIGVLLDTNLYFWYEGLDH 180
DB 121 sswaettywispgipetkvgdmcvynwqyllcswkpgigvlldtnnlyfwyegldl 180
QY 181 ALOQVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQOLNIVKPLP 240
DB 181 alqcvdyikadgqnlgcrfpyleasdykdfyicvngssenkprrssytfqlqnvkplp 240
QY 241 PYYLFTTRESSCEIKLWSIPLGPAPCFDYEIREDDTTLVTATVENETYTLTKTTNE 300
DB 241 pylvlftressceiklwgipgpaprcfdyeyreiddttlvtatvenetytlktttne 300
QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQCEGEDLS 337
DB 301 trqlcfvvrskvnlycsddgiwsewsdkqcegedls 337

RESULT 11
AAW56261
ID AAW56261 standard; Protein; 315 AA.

AC AAW56261;
XX
XX
DT 16-SEP-1998 (first entry)
XX
DE Mature interleukin-13 binding protein.
XX
XX Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.
XX
OS Homo sapiens.
XX
PN WO9810638-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-AU00591.
XX
PR 27-FEB-1997; 97AU-0005374.
XX
PR 10-SEP-1996; 96AU-0002262.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
PI
XX

DR WPI; 1998-207062/18.
DR N-PSDB; AAV22702.
XX
PT New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX
PS Disclosure; Page 55-56; 69pp; English.
XX
CC The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX
SQ Sequence 315 AA;

Query Match 92.1%; Score 1725; DB 19; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPDPDFEIVDPGVLGYLQWOPPLSLDHFKECTVEYELKYNIGSETWKTITTKN 88
DB 1 eikvnpdpdfivdpgylylqwgppslidhfkeytveyelkynigsetwktitkn 60
QY 89 LHYKDGFDLNGKIEAKIHTLLPQCTNGSEVQSSWAETTYWISPOGIPETKVDQMCVY 148
DB 61 lhykdgfdlnkgeakihltllpwqctngsevgsswaettywispgipetkvgdmcvyy 120
QY 149 NWQYLLCSWPKGIGVLLDTNLYFWYEGLDHALQCVDYIKADGONIGCRFPYLEASDYK 208
DB 121 nwqyllcswkpgigvlldtnnlyfwyegldhalqcvdyikadgqnlgcrfpyleasdyk 180
QY 209 DFYICVNGSSSENKPIRSSYTFQOLNIVKPLPVPVLTFTRESSCEIKLWSIPLGPAP 268
DB 181 dfyicvngssenkprrssytfqlqnvkplppylvlftressceiklwsipgipar 240
QY 269 CFDYEIREDDTTLVTATVENETYTLTKTNETQLCFVVRKVNICYSDGDIWSEWSK 328
DB 241 cfdyeyreiddttlvtatvenetytlkttnetqlcfvvrskvnlycsddgiwsewsdk 300
QY 329 QCWEGEDLS 337
DB 301 qcwgedls 309

RESULT 12
AAW56260
ID AAW56260 standard; Protein; 359 AA.

AC AAW56260;
XX
XX
DT 16-SEP-1998 (first entry)
XX
DE Construct containing mature interleukin-13 binding protein.
XX
KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
KW autoimmune disease; antibody; immunotherapy.
XX
OS Homo sapiens.
XX
PN WO9810638-A1.
XX
PD 19-MAR-1998.
XX
PF 10-SEP-1997; 97WO-AU00591.
XX
PR 27-FEB-1997; 97AU-0005374.
PR 10-SEP-1996; 96AU-0002262.
XX


```
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX WPI; 1998-207062/18.
DR N-PSDB; AAV22701.
XX New isolated interleukin-13 binding protein - used to develop
PT products for therapy e.g. for allergic conditions such as asthma or
PT for diagnosis or detection
XX Example 14; Page 52-53; 69pp; English.
XX The IL-13 binding protein and related therapeutic molecules can be used
CC in the antagonism of at least one IL-13 activity. They can be used for
CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.
XX Sequence 359 AA;
XX
XX Query Match 92.1%; Score 1725; DB 19; Length 359;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-161;
XX Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 29 EIKVNPDDFEIVDPGYLGILYLQWPPSLDHFKECVNELKYNIGSETWKIIITKN 88
Db 45 eikvnppqdfelvdpgylylgwppslidhfkectveylkynigsetwktitkn 104
Qy 89 LHYKDGFDLNGIEAKIHTLLPWOCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCVY 148
Db 105 lhykdgfdlنگieakihllpwqctngsevgsswaettywispgipetkvqdmndcvy 164
Qy 149 NWQYLLCSWKPGIGVLLDTNVLFWYEGDLHALQCVDIKADGONIGCRFPYLEADYK 208
Db 165 nwqyllcswkpgigvlltdnvnlfwyegdlhalqcvdyikadggnigcrfpyleasyk 224
Qy 209 DFYICVNGSSENKPIRSSVFTFOLNIVKPLPPVYLTFTRESSCEIKLWSIPGLPIPAR 268
Db 225 dfyicvngssenknprssyftfqlnkvplppvytftressceiklwsipglpar 284
Qy 269 CPDYEIREDDTTLVATVENETYLKTTNETRLCFVRSKVNICYSDDGIMSEWSDK 328
Db 285 cfdyeireddttlvatvenetyllkttnetrlcfcvrskvnicycsddgimsewsdk 344
Qy 329 QCWEGEDLS 337
Db 345 qcwegedis 353
XX
XX RESULT 13
XX AAW36616
XX ID AAW36616 standard; Protein; 372 AA.
XX AC AAW36616;
XX XX
XX 30-MAR-1998 (first entry)
XX Celebus macaque zcytor2 protein.
XX
XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
XX infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX
XX Macaque sp.
XX Key Location/Qualifiers
XX Protein 1..372
XX /label= Zcytor2
XX /note= "partial protein sequence"
XX
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PN WO9733913-A1.
XX 18-SEP-1997.
XX 12-MAR-1997; 97WO-US04043.
XX 13-MAR-1996; 96US-0013345.
XX (ZYMO ) ZYMOGENETICS INC.
XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
XX O'Hara PJ;
XX WPI; 1997-470820/43.
XX N-PSDB; AAT96784.
XX New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
XX Example 4; Page 56-57; 79pp; English.
XX This sequence represents a novel ligand-binding receptor, Zcytor2,
XX which shares homology with cytokine receptors and is isolated from
XX testis tissue obtained from a Celebus macaque. The resulting polypeptide
XX is a receptor for cytokines (particularly interleukin-13) and is
XX expressed on the surface of testicular cells, probably being involved in
XX spermatogenesis. It can be used to detect ligands promoting proliferation
XX and/or differentiation of such cells in cultures and may also be used to
XX treat infertility. Antagonists of this receptor may be used to
XX characterise ligand-receptor interactions and as male-specific
XX contraceptives. By blocking the action of IL-13, receptor antagonists and
XX ligand-binding this receptor can also be used to modulate immune
XX function, e.g. in allergy and asthma, as a diagnostic to determine
XX circulating levels of ligand and also to isolate and purify ligands.
XX Antibodies can be used to assay circulating receptor (an abnormal level
XX may be indicative of disease such as cancer), for labelling cells that
XX express the receptor, and therapeutically as antagonist.
XX Sequence 372 AA;
XX
XX Query Match 91.7%; Score 1718; DB 18; Length 372;
XX Best Local Similarity 93.5%; Pred. No. 1.1e-160;
XX Matches 314; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
XX
Qy 1 MAFVCLATGCLYFLISTFGCTSSDTEIKVNPQDFEIVDPGYLGILYLQWQPPSLD 60
Db 1 mafvylairclctflistftgyststsdteikvnpqdfelvdpgylylgwqppslid 60
Qy 61 HFKECTVEVELKYRNIGSETWKTITTKNLHYKDGFDLNGIEAKIHTLLPWOCTNGSEVO 120
Db 61 nfkectveyelkynigsetwtitknlhykdgfdlنگieakihllpwqctngsevg 120
Qy 121 SSWAETTYWISPOGIPETKVQDMDCVYVNWQYLLCSWKPGIGVLLDTNVLFWYEGDLH 180
Db 121 sswaeatywispgipetkvqdmndcvynwqyllcswkpgigvlltdnvnlfwyegldr 180
Qy 181 ALQCVDIYKADGONIGCRFPYLEADYKDFYICVNGSSENKPIRSSYFTFQONIVKPLP 240
Db 181 alqcvdyikvdggnigcrfpyleasydkdfyicvngssenkprrssyftfqinivkplp 240
Qy 241 PVLVFTFTRESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVATVENETYLKTTNE 300
Db 241 pvlclctgeslyelklsipglpircfveyelreddttlvatvenetyllkttne 300
Qy 301 TROLCFVRSKVNICYSDDGIMSEWSDKQCWEGEDL 336
Db 301 trqlcfvrskvnicycsddgimsewsdkqcwevedl 336
XX
XX RESULT 14
XX AAW35294
```

AAW35294 standard; Protein; 383 AA.
AAW35294;
27-MAR-1998 (first entry)
Murine IL-13 binding chain of the IL-13 receptor.
Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
allergy; asthma; immune complex disorder.
Mus sp.
Key Location/Qualifiers
Peptide 1..21
Protein /label= signal_sequence
22..383 /note= "putative"
Domain /label= mature_protein
22..334
Domain /label= extracellular_domain
335..356
Domain /label= transmembrane_domain
357..383
Domain /label= intracellular_domain
WO9731946-A1.
04-SEP-1997.
28-FEB-1997; 97WO-US03124.
01-MAR-1996; 96US-0609572.
(GEMY) GENETICS INST INC.
Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
Wood C;
WPI; 1997-448632/41.
N-PSDB; AAT75213.
New nucleic acid encoding interleukin-13 receptor binding chain and
transformed cells - proteins, antibodies and inhibitors, for
treating immunoglobulin E-mediated diseases, e.g. Graves disease,
and in diagnosis
Claim 11; Pages 30-31; 49pp; English.
The present sequence represents the murine interleukin-13 (IL-13) binding
chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
mediator of the known biological activities of IL-13. Recombinant
IL-13bc proteins, and antibodies raised against them, are used to
inhibit the binding of IL-13 to its receptor. They are particularly used
to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
They are also used to treat immune deficiency (particularly in
haematopoietic progenitor cells), cancer etc., and to increase macrophage
activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
with such activity is combined with IL-13bc and the mixture applied,
in vivo, to a cell expressing at least one chain of the IL-13 receptor
other than IL-13bc. IL-13bc can also be used in diagnosis to detect
expression of IL-13, its receptor or binding chain, and to raise specific
antibodies which may be useful for treating some tumours.
Sequence 383 AA;

Query Match 63.2%; Score 1184; DB 18; Length 383;
Best Local Similarity 64.0%; Pred. No. 3.8e-108;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCLYTELISTFGCTSSDTEIKVNPQDFEIVDPGLYGLYLQWOPPLSLD 60
DB 1 mafv--hircfcilctitgys---leikvnpqdfelldpglylylqkppvvie 54
QY 61 HFKECTVEYELKYRNIGSEWKTITITNHLHYKDGFDLNKGIEAKIHLLPWQCTNGSEVQ 120
DB 55 kfgctleyelkyrnvdswktititnlykdgfdlnkglegkirthlsehtngsevg 114
QY 121 SSWAETTYWISPOGIPETKVDMDCVVYNNQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
DB 115 spwleasygdegslctkqgmckciyynwqylvcskpgktvysdntnytmffvegldh 174
QY 181 ALQCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSENKPIRSYFTFOLQNVKPLP 240
DB 175 alqcadyldqdeknvgcklnldssdykdficvngssklepirssyvtvqlnkvplp 234
QY 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYETIEIREDDTTLVTAVENTYTLKTTNE 300
DB 235 peflhsvensidirmkwtstpggpiprcycteyeiaveddiswesatdkndmkikrrane 294
QY 301 TROLCFVVRKVNLYCSDGDIWSEMSDKQWEG 333
DB 295 sedicffvrckvnllycaddgiwsewseeecweg 327
RESULT 15
AAV95295
ID AAV95295 standard; Protein; 383 AA.
XX AC AAV95295;
XX DT 12-SEP-2000 (first entry)
XX DE IL-13 binding chain of mouse IL-13 receptor.
XX KW Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; antiallergic;
KW antiinflammatory; antiasthmatic; vaccine.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
22..383
FT Domain /note= "mature protein"
22..334
FT FT /note= "extracellular domain; a polypeptide
comprising amino acids 22-334 is
specifically claimed in Claim 11(b)"
FT Domain 335..356
FT /note= "transmembrane domain"
FT Domain 357..383
FT FT /note= "intracellular domain; a polypeptide
comprising amino acids 257-383 is
specifically claimed in Claim 11(c)"
XX WO200036103-A1.
XX 22-JUN-2000.
XX 13-DEC-1999; 99WO-US29493.
XX 14-DEC-1998; 98US-0211335.
XX (GEMY) GENETICS INST INC.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
XX Wills-Karp M;
XX

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:08:36 ; Search time 35.33 Seconds
(without alignments)
196.404 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_337

Perfect score: 1873

Sequence: 1 MAFVCLAIGCLYTLFLISTTF.....DDGIWSEWSKQWEGEDLS 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1873	100.0	380	1	US-08-609-572-4
2	1873	100.0	380	4	US-08-841-751-4
3	1873	100.0	380	4	US-08-846-340-4
4	1184	63.2	383	1	US-08-609-572-2
5	1184	63.2	383	4	US-08-841-751-2
6	1184	63.2	383	4	US-08-846-340-2
7	293.5	15.7	420	1	US-07-757-390-13
8	293.5	15.7	420	1	US-08-442-282-13
9	293.5	15.7	420	1	US-08-442-281-13
10	293.5	15.7	420	1	US-08-939-727-13
11	293	15.6	313	3	US-08-836-561-106
12	292.5	15.6	396	1	US-07-757-390-14
13	292.5	15.6	396	1	US-08-442-282-14
14	292.5	15.6	396	1	US-08-442-281-14
15	292.5	15.6	396	2	US-08-939-727-14
16	292	15.6	335	1	US-07-947-130-2
17	292	15.6	335	1	US-08-421-822-2
18	292	15.6	335	1	US-08-421-823-2
19	285	15.2	427	4	US-08-969-125-9
20	229	12.2	315	1	US-07-757-390-8
21	229	12.2	315	1	US-08-442-282-8
22	229	12.2	315	1	US-08-442-281-8
23	229	12.2	315	2	US-08-939-727-8
24	229	12.2	332	1	US-07-757-390-7
25	229	12.2	332	1	US-08-442-282-7
26	229	12.2	332	1	US-08-442-281-7
27	229	12.2	332	2	US-08-939-727-7

Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 11, Appli
Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-609-572-4
; Sequence 4, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-609-572-4

Query Match 100.0%; Score 1873; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.1e-186;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFLISTTFCTSSSTKVNPPQDFEIVDPGVLGYLQWQPLSLD 60

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Db 1 MAFVCLAIGCLYTLSTTTCGSSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
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Db 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKEAKIHTLLPWOCTNGSEVQ 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNYNLFYWEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNYNLFYWEGLDH 180
QY 181 ALQCVDIYKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 ALQCVDIYKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
QY 241 PVYLFTFRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNE 300
Db 241 PVYLFTFRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNE 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLS 337
Db 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLS 337
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RESULT 2
US-08-841-751-4
; Sequence 4, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-841-751-4
```

Query Match 100.0%; Score 1873; DB 4; Length 380;

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Best Local Similarity 100.0%; Pred. No. 3.1e-186;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTLSTTTCGSSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTLSTTTCGSSSDTEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
QY 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKEAKIHTLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKEAKIHTLLPWOCTNGSEVQ 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNYNLFYWEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDTNYNLFYWEGLDH 180
QY 181 ALQCVDIYKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 ALQCVDIYKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
QY 241 PVYLFTFRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNE 300
Db 241 PVYLFTFRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNE 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLS 337
Db 301 TROLCFVVRSKVNIYCSDDGIWSEWSKOCWEGEDLS 337
RESULT 3
US-08-846-340-4
; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

US-08-846-340-4

Query Match 100.0%; Score 1873; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.1e-186;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAGCGLYTLFTTFCGTSSTDEIKVNPQDPFEIYVDPGVLGYLYLQWOPPLSLD 60
Db 1 MAFVCLAGCGLYTLFTTFCGTSSTDEIKVNPQDPFEIYVDPGVLGYLYLQWOPPLSLD 60

Qy 61 HFKECTVEYELKYRNIGSETWKTITITKLNHYKDGFDLNGKTEAKIHTLLPQCTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTITITKLNHYKDGFDLNGKTEAKIHTLLPQCTNGSEVQ 120

Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNWQYLLCSWKPGIGVLLDTNINFLFYWYEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVDMDCVYNNWQYLLCSWKPGIGVLLDTNINFLFYWYEGLDH 180

Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240
Db 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240

Qy 241 PVLTFTRSSCEIKLWSIPLGPIPARCFDYIEIREDDTTLVTATVENETYLKTINE 300
Db 241 PVLTFTRSSCEIKLWSIPLGPIPARCFDYIEIREDDTTLVTATVENETYLKTINE 300

Qy 301 TROLCFVVRKVNIIYCSDDGIWSEWSKQCEGDL 337
Db 301 TROLCFVVRKVNIIYCSDDGIWSEWSKQCEGDL 337

RESULT 4

US-08-609-572-2
; Sequence 2, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-609-572-2

Query Match 63.2%; Score 1184; DB 1; Length 383;
Best Local Similarity 64.0%; Pred. No. 1.1e-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

Qy 1 MAFVCLAGCGLYTLFTTFCGTSSTDEIKVNPQDPFEIYVDPGVLGYLYLQWOPPLSLD 60
Db 1 MAFV--HRCCLCFLITITIGYS----LEIKVNPQDPFEIILDPGLLYLQWKPVPVIE 54

Qy 61 HFKECTVEYELKYRNIGSETWKTITITKLNHYKDGFDLNGKTEAKIHTLLPQCTNGSEVQ 120
Db 55 KFKGCTLEYELKYRNIVSDSKWTITITRNLKYKDGFDLNGKTEGKIRTHLSEHCTNGSEVQ 114

Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNWQYLLCSWKPGIGVLLDTNINFLFYWYEGLDH 180
Db 115 SPWTEASYGISDEGSLETKIQDMKCIYNNWQYLLCSWKPGIKTVSDNTNMTFFWYEGLDH 174

Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240
Db 175 ALQCADYLOHDEKNGVCKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTVFOLQNIKPLP 234

Qy 241 PVLTFTRSSCEIKLWSIPLGPIPARCFDYIEIREDDTTLVTATVENETYLKTINE 300
Db 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDMKLKRANE 294

Qy 301 TROLCFVVRKVNIIYCSDDGIWSEWSKQCEWEG 333
Db 295 SEDLCFFVRKVNIIYCADDDGIWSEWSEEECEWEG 327

RESULT 5

US-08-841-751-2
; Sequence 2, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:

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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 383 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
US-08-841-751-2

Query Match          63.2%; Score 1184; DB 4; Length 383;
Best Local Similarity 64.0%; Pred. No. 1.le-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60
Db 1 MAFV--HIRCLFCILLCTITGYS----LEIKVNPQDFEILDPLGLGLGYLYLQWPPVVE 54

QY 61 HFECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKEAKIHTLLPHQCTNGSEVQ 120
Db 55 KFGCTLEYELKYRNVDSDSWKTIITRNLHYKDGFDLNGKEGKIRTHLSEHCTNGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPVGIGVLLDTNLYNLFYWEGLDH 180
Db 115 SPWIEASGIGDESLETKIDMKCIYNNQYLLCSWKPVGITVSDNTYTFWYEGLDH 174

QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSKNPIRSSYFTFOLQNVKPLP 240
Db 175 ALQCADYLQHDKNVGVKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTFVOLFQNVKPLP 234

QY 241 PVLFTFRESCEIKLWSIPGLPIPARCFDYEIEIRDDTTLTAVENETYLKTTNE 300
Db 235 PEFHLISVENSIDIRMKWSTPGGPIPRCYTYEIVREDDISWESATDKNDMKLKRANE 294

QY 301 TROLCFVVRKSVNIYCSDDGIWSEMSDKQWEG 333
Db 295 SEDLCFFVRCKVNIYCADDGIWSEMSSEECWEG 327

RESULT 6
US-08-846-340-2
; Sequence 2, Application US/08846340
; Patent No. 6248714
;
GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A. 32,724
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: G15268
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 383 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
US-08-846-340-2

Query Match          63.2%; Score 1184; DB 4; Length 383;
Best Local Similarity 64.0%; Pred. No. 1.le-114;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;

QY 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60
Db 1 MAFV--HIRCLFCILLCTITGYS----LEIKVNPQDFEILDPLGLGLGYLYLQWPPVVE 54

QY 61 HFECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKEAKIHTLLPHQCTNGSEVQ 120
Db 55 KFGCTLEYELKYRNVDSDSWKTIITRNLHYKDGFDLNGKEGKIRTHLSEHCTNGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPVGIGVLLDTNLYNLFYWEGLDH 180
Db 115 SPWIEASGIGDESLETKIDMKCIYNNQYLLCSWKPVGITVSDNTYTFWYEGLDH 174

QY 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSKNPIRSSYFTFOLQNVKPLP 240
Db 175 ALQCADYLQHDKNVGVKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTFVOLFQNVKPLP 234

QY 241 PVLFTFRESCEIKLWSIPGLPIPARCFDYEIEIRDDTTLTAVENETYLKTTNE 300
Db 235 PEFHLISVENSIDIRMKWSTPGGPIPRCYTYEIVREDDISWESATDKNDMKLKRANE 294

QY 301 TROLCFVVRKSVNIYCSDDGIWSEMSDKQWEG 333
Db 295 SEDLCFFVRCKVNIYCADDGIWSEMSSEECWEG 327

RESULT 7
US-07-757-390-13
; Sequence 13, Application US/07757390
; Patent No. 5453491
;
GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
;
; TELECOMMUNICATION INFORMATION:
```



```
;
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-757-390-13

Query Match      15.7%; Score 293.5; DB 1; Length 420;
Best Local Similarity 28.1%; Pred. No. 3.4e-22;
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps 13;

Qy 27 DTEIKVNPQDFEIVDPGILGYLYLQWQPPSLSDHFRECTVEYELKYRNIGSETWKTIIIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIIT 82
Qy 87 KNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKYQDMDCV 146
Db 83 ES---KCVTIHLKGFSAVRILQ---NDHSLASSWASAEHL-APPGSPGTSVNNLTCT 135
Qy 147 -----YNNQYLL-CSWKPGIGVLLDTNINLFY----WYEGLDHALQCVDYIKAD 191
Db 136 TTTTNDNYSRLRSYQVSLHCTWLVGTDAPEYQFLYRYGSWTE-----ECQEYSKDT 189
Qy 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
Db 190 LGRNIACFPRTFILSKGRDWLAVLVNGSSKHSAIRPDPQLFALHAIDQINPPLNVTAEI 249
Qy 249 ESSCEIKLWSIPGLPIPARCFDYEIEIREDDTTLVTATVENETTYTLKTTNETQLCFV 308
Db 250 EGT-RLSQWEKPSAFPIHCFDYEIVKHTRNGYLVQIEKLTNAFISIIDLSKYDVQV 308
Qy 309 RSKVNIYCSDDGIWSEWSDKOCWEGED 335
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGN 334

RESULT 8
US-08-442-282-13
; Sequence 13, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/442.282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-282-13

Query Match      15.7%; Score 293.5; DB 1; Length 420;
Best Local Similarity 28.1%; Pred. No. 3.4e-22;
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps 13;

Qy 27 DTEIKVNPQDFEIVDPGILGYLYLQWQPPSLSDHFRECTVEYELKYRNIGSETWKTIIIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIIT 82
Qy 87 KNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKYQDMDCV 146
Db 83 ES---KCVTIHLKGFSAVRILQ---NDHSLASSWASAEHL-APPGSPGTSVNNLTCT 135
Qy 147 -----YNNQYLL-CSWKPGIGVLLDTNINLFY----WYEGLDHALQCVDYIKAD 191
Db 136 TTTTNDNYSRLRSYQVSLHCTWLVGTDAPEYQFLYRYGSWTE-----ECQEYSKDT 189
Qy 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
Db 190 LGRNIACFPRTFILSKGRDWLAVLVNGSSKHSAIRPDPQLFALHAIDQINPPLNVTAEI 249
Qy 249 ESSCEIKLWSIPGLPIPARCFDYEIEIREDDTTLVTATVENETTYTLKTTNETQLCFV 308
Db 250 EGT-RLSQWEKPSAFPIHCFDYEIVKHTRNGYLVQIEKLTNAFISIIDLSKYDVQV 308
Qy 309 RSKVNIYCSDDGIWSEWSDKOCWEGED 335
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGN 334

RESULT 9
US-08-442-281-13
; Sequence 13, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/442.281
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-281-13

Query Match 15.7%; Score 293.5; DB 1; Length 420;
Best Local Similarity 28.1%; Pred. No. 3.4e-22;
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps 13;

QY 27 DTEIKVNPDPQFEIVDPGILGYLYLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
DB 25 DEKISLLPPVNFETIKVYG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
QY 87 KNLHYKDGFDLKNKIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKYQDMDCV 146
DB 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSPGTSVVNLCT 135
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF----WYEGDLHALQCVDIYKAD 191
DB 136 TTTTNDYSLRSYQVSLHCTWLVGTDPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -QONIGCRFP--YLEASDYKDFYICVNGSSNKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
DB 190 LGRNIACWFPTFTLSKGRDLAVLVNGSSKHSAIRPFDQLFALHAIQINPLNVTAEI 249
QY 249 ESSCEIKLWSIPLGPPIPARCFDYEIREDDTTLVATVENETTYTLKTNETQLCFV 308
DB 250 EGT-RLSIQWEKPVSAFPIHCFDYEKIHNRNGYLQTEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSESKOCWEGED 335
DB 309 RAAVSMCREAGLWSEWS-QPIYVGN 334

RESULT 10
US-08-939-727-13
; Sequence 13, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-939-727-13

Query Match 15.7%; Score 293.5; DB 2; Length 420;
Best Local Similarity 28.1%; Pred. No. 3.4e-22;
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps 13;

QY 27 DTEIKVNPDPQFEIVDPGILGYLYLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
DB 25 DEKISLLPPVNFETIKVYG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
QY 87 KNLHYKDGFDLKNKIEAKIHTLLPWQCTNGSEVOSSWAETTYWISPOGIPETKYQDMDCV 146
DB 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSPGTSVVNLCT 135
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF----WYEGDLHALQCVDIYKAD 191
DB 136 TTTTNDYSLRSYQVSLHCTWLVGTDPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -QONIGCRFP--YLEASDYKDFYICVNGSSNKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
DB 190 LGRNIACWFPTFTLSKGRDLAVLVNGSSKHSAIRPFDQLFALHAIQINPLNVTAEI 249
QY 249 ESSCEIKLWSIPLGPPIPARCFDYEIREDDTTLVATVENETTYTLKTNETQLCFV 308
DB 250 EGT-RLSIQWEKPVSAFPIHCFDYEKIHNRNGYLQTEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSESKOCWEGED 335
DB 309 RAAVSMCREAGLWSEWS-QPIYVGN 334

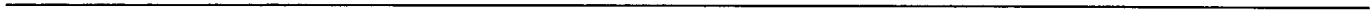
RESULT 11
US-08-836-561-106
; Sequence 106, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiko
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANAI, No. 6018032uo
; APPLICANT: TAKATSU, Kiyoshi
; TITLE OF INVENTION: Antibody Against Human Interleukin-5
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
```


; Sequence 14, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-939-727-14

Query Match 15.6%; Score 292.5; DB 2; Length 396;
Best Local Similarity 27.8%; Pred. No. 4e-22;
Matches 91; Conservative 58; Mismatches 143; Indels 35; Gaps 13;

Qy	27	DTEIKVNPDPQFEIVDPGYLVYLQWQPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
Db	25	DEKISLLFPVNETIKVTG-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
Qy	87	KNLHYKDGFDLNGKEAKIHTLLPQCTNGSEVOSSMAETTYWISPGQIPETKYQDMDCV 146
Db	83	ES---KCVTILHKGFSAVRLIQ---NDHSLASSWASAEHL-APPGSPGTSIVNLFTCT 135
Qy	147	-----YYNQYLL-CSWKPGIGVLLDTNLYF----WYEGDLHALQCVDYIKAD 191
Db	136	TNTTENDNYSRLRSQVSLHCTWLVTGDPEDTQYFLYYRYGSWTE-----ECQEYSKDT 189
Qy	192	-QNGIGCRFP--YLEADSKDFYICVNGSSSENKPIRSSYFTFOLQNIKVPPLPPVLTETR 248
Db	190	LGRNIACWFPPTFILSKGRDMLAVLVNGSSKHSAIRPFDQLFALHAIQINPPLNVTAEI 249
Qy	249	ESSCEIKLKWISPLGPIPARCFYEIEIREDDTTLTATVENETYYTLKTTNETRQLCFWV 308
Db	250	EGT-RLSIQWEKPKVSAPFIHCFDYEKVIHNTNRNGYLQIEKLTNAFISIIDLSKYDVQV 308
Qy	309	RSKVNICYSDDGINSEWSKOCWEGED 335
Db	309	RAAVSSMCREAGLWSEWS-QPIYVGN 334

Search completed: September 1, 2001, 19:08:37
Job time: 164 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:58 ; Search time 24.79 Seconds
(without alignments)
525.094 Million cell updates/sec

Title: US-09-077-817-2

Perfect score: 2104

Sequence: 1 MAFVCLAIGCLYFLISTTF.....ILLRKNTPYKMIPEFFCDT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	2104	100.0	1 IL32_HUMAN	Q14627 homo sapien
2	310.5	14.8	1 IL5R_HUMAN	Q01344 homo sapien
3	298	14.2	1 IL31_MOUSE	O09030 mus musculus
4	295.5	14.0	1 IL31_HUMAN	P78552 homo sapien
5	263	12.5	1 PRLR_CHICK	Q04594 gallus gall
6	247	11.7	1 IL5R_MOUSE	P21183 mus musculus
7	238	11.3	1 PRLR_MELGA	Q91094 meleagris g
8	220	10.5	1 CYRG_HUMAN	P31785 homo sapien
9	216.5	10.3	1 PRLR_COLLI	Q90374 columba liv
10	212.5	10.1	1 CYRG_MOUSE	P34902 mus musculus
11	208	9.9	1 CYRG_CANFA	P40321 canis fam
12	195	9.3	1 IL3B_MOUSE	P26954 mus musculus
13	189.5	9.0	1 CYRG_BOVIN	Q95118 bos taurus
14	178.5	8.5	1 CYRG_MOUSE	P32927 homo sapien
15	173.5	8.2	1 CYRG_MOUSE	P26955 mus musculus
16	165	7.8	1 PRLR_BOVIN	Q28172 bos taurus
17	165	7.8	1 PRLR_RAT	P05710 rattus norv
18	159	7.6	1 PRLR_MOUSE	Q08501 mus musculus
19	151	7.2	1 PRLR_HUMAN	P16471 homo sapien
20	151	7.2	1 IL2S_HUMAN	Q09665 homo sapien
21	150.5	7.2	1 IL6B_MOUSE	Q00560 mus musculus
22	150	7.1	1 PRLR_CEREL	Q28235 cervus elap
23	149	7.1	1 PRLR_RABIT	P14787 oryctolagus
24	142.5	6.8	1 GMCR_HUMAN	P15509 homo sapien
25	138	6.6	1 IL3R_HUMAN	P26951 homo sapien
26	134.5	6.4	1 LIFR_MOUSE	P42702 homo sapien
27	131.5	6.2	1 PRLR_ORENI	Q91513 oreochromis
28	128	6.1	1 IL2S_MOUSE	P97378 mus musculus
29	126.5	6.0	1 IL6B_HUMAN	P40189 homo sapien
30	120.5	5.7	1 GCSR_HUMAN	Q99062 homo sapien
31	113.5	5.4	1 LEPR_HUMAN	P48357 homo sapien
32	112.5	5.3	1 PTPI_DROME	P35992 drosophila
33	109.5	5.2	1 IL6B_RAT	P40190 rattus norv

ALIGNMENTS

RESULT	ID	IL32_HUMAN	STANDARD;	PRT;	380 AA.
AC	Q14627	O00667;			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	30-MAY-2000	(Rel. 39, Last annotation update)			
DE	INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13 DE BINDING PROTEIN).				
GN	IL13RA2 OR IL13R.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Renal cell carcinoma;				
RX	MEDLINE=96279273; PubMed=8663118;				
RA	Caput D., Laurent P., Kagnad M., Lelias J.M., Lefort S., Vita N., Ferrara P.;				
RT	"Cloning and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha chain.";				
RL	J. Biol. Chem. 271:16921-16926(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Testis;				
RA	Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H., Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;				
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=97321053; PubMed=9177784;				
RA	Guo J., Apiou F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;				
RT	"Chromosome mapping and expression of the human interleukin-13 receptor.";				
RL	Genomics 42:141-145(1997).				
CC	-1- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13 (IL-13). BUT NOT TO IL-4.				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.				
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL;	X95302;	CAA64617.1;	-;	
DR	EMBL;	U70981;	AAB17170.1;	-;	
DR	EMBL;	Y08768;	CAA70021.1;	-;	
DR	MTM;	300130;	-;	-;	

P10912 homo sapien
P40223 mus musculus
P79108 bos taurus
Q28575 ovis aries
P04884 vesicular s
P42703 mus musculus
P19756 sus scrofa
P19941 oryctolagus
Q62959 rattus norv
P14753 mus musculus
P16310 rattus norv
P48356 mus musculus

34 107.5 5.1 638 1 GHR_HUMAN
35 107.5 5.1 837 1 GCSR_MOUSE
36 107 5.1 634 1 GHR_BOVIN
37 106 5.0 634 1 GHR_SHEEP
38 105 5.0 511 1 VGLG_VSVO
39 104.5 5.0 1092 1 LIFR_MOUSE
40 102.5 4.9 638 1 GHR_PIG
41 101.5 4.8 638 1 GHR_RABIT
42 99.5 4.7 1162 1 LEPR_RAT
43 99 4.7 507 1 EPOR_MOUSE
44 99 4.7 638 1 GHR_RAT
45 98.5 4.7 1162 1 LEPR_MOUSE

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DR InterPro: IPR001777; -
DR InterPro: IPR002465; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT DISULFID 184 197
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B562C887 CRC64;

Query Match 100.0%; Score 2104; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.4e-164;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTELSTFCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
DB 1 MAFVCLAIGCLYTELSTFCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
DB 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHLLPWQCTNGSEVQ 120
QY 121 SSWAETTYWISQGIPTKVDMDCVYNNQYLLCSKWKPGIGVLLDTNLYNLFYWEGLDH 180
DB 121 SSWAETTYWISQGIPTKVDMDCVYNNQYLLCSKWKPGIGVLLDTNLYNLFYWEGLDH 180
QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNVKPLP 240
DB 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNVKPLP 240
QY 241 PVYLTFRESSECEIKLWSIPGLPIPARCFDYEIEIRDDTTLTAVENETYTLKTTNE 300
DB 241 PVYLTFRESSECEIKLWSIPGLPIPARCFDYEIEIRDDTTLTAVENETYTLKTTNE 300
QY 301 TRQLCFVVRSVKNIYCSDDGIWSEWSKQCEGEDLSKTLRLFWLPGFLLIVIVFTG 360
DB 301 TRQLCFVVRSVKNIYCSDDGIWSEWSKQCEGEDLSKTLRLFWLPGFLLIVIVFTG 360
QY 361 LLLRKPNTYKMPIEFFCDT 380
DB 361 LLLRKPNTYKMPIEFFCDT 380

RESULT 2
IL5R_HUMAN STANDARD; PRT; 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125
DE ANTIGEN).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;
RT "Molecular basis of the membrane-anchored and two soluble isoforms of
RT the human interleukin 5 receptor alpha subunit.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
RN [3]
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=92005689; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of
RT an IL5-specific alpha chain and a beta chain shared with the receptor
RT for GM-CSF.";
RL Cell 66:1175-1184(1991).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -1- DATABASE: NAME=PROW; NOTE=cd guide cdw125.htm;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M96652; AAA59152.1; -
DR EMBL: M96651; AAA59151.1; -
DR EMBL: M75914; AAA36110.1; -
DR EMBL: A36249; CAA01793.1; -
DR EMBL: A24587; CAA01731.1; -
DR EMBL: A36251; CAA01794.1; -
DR PIR: A40267; A40267.
DR MIM: 147851; -
DR InterPro: IPR000950; -
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT DOMAIN 21 342 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 343 362 POTENTIAL.
FT DOMAIN 363 420 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 333 335 NDE -> FSR (IN SOLUBLE ISOFORM S1).
FT VARSPPLIC 336 420 MISSING (IN SOLUBLE ISOFORM S1).
FT VARSPPLIC 333 333 N -> K (IN SOLUBLE ISOFORM S2).
FT VARSPPLIC 334 420 MISSING (IN SOLUBLE ISOFORM S2).
SQ SEQUENCE 420 AA; 47700 MW; 420881FEC6B51700 CRC64;

Query Match 14.8%; Score 310.5; DB 1; Length 420;
Best Local Similarity 26.6%; Pred. No. 3.9e-18;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIT 86
DB 25 DEKISLPPVNFITKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82

```


IL4R alpha of a functional IL-4/IL-13 receptor complex.";
 [2] FERS Lett. 401:163-166(1997).
 RN
 RC TISSUE-B-cell;
 RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
 RA Jeunin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
 RA Eugster H.P., Bonnefoy J.Y.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE-T-cell;
 RX MEDLINE-97067184; PubMed-9910586;
 RA Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S.,
 RA Leonard W.J.;
 RT "cDNA cloning and characterization of the human interleukin 13
 receptor alpha chain.";
 RL J. Biol. Chem. 271:29265-29270(1996).
 [4]
 RN
 RP SEQUENCE FROM N.A.
 RA Wada M., Hisano T., Kuwano M.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
 ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
 ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
 CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
 GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.
 CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
 IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER,
 SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
 KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
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 EMBL; Y10659; CAA71669.1; -
 EMBL; Y09328; CAA70508.1; -
 EMBL; U62858; AAB37127.1; -
 EMBL; U81379; AAD00510.3; -
 HSSP; P31785; 1ILN.
 MIM; 300119; -
 InterPro; IPR001777; -
 Pfam; PF00041; fn3; 1.
 PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 427
 FT DOMAIN 22 343
 FT TRANS 344 367
 FT TRANS 368 427
 FT DOMAIN 39 102
 FT DISULFID 46 95
 FT DISULFID 134 144
 FT DISULFID 173 185
 FT CARBOHYD 37 37
 FT CARBOHYD 61 61
 FT CARBOHYD 105 105
 FT CARBOHYD 138 138
 FT CARBOHYD 157 157
 FT CARBOHYD 235 235
 FT CARBOHYD 265 265
 FT CARBOHYD 293 293
 FT CARBOHYD 329 329

 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 130 130 T -> I (IN REF. 3).
 FT CONFLICT 358 358 G -> D (IN REF. 3).
 SQ SEQUENCE 427 AA; 48759 MW; 5983B3E8F554107B CRC64;
 Query Match 14.0%; Score 295.5; DB 1; Length 427;
 Best Local Similarity 26.0%; Pred. No. 6.7e-17;
 Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;
 QY 11 LYTELSTFTGCTSSSTTEIKVNPDPQFEIVDPGYLYLQWOPPLSLDHFKECTVEY- 69
 DB 10 LWALLLCAGGGGGGAAPTETQPPVTLNLSVENLCTVIWTNPPGAS--SNCSLWYF 67
 QY 70 ---ELAYRNIGSETWKTIIITKNLHYKDGFDLNGIEAKIHTLLPWQC-TNGSEVQSSWA 124
 DB 68 SHFGDKQDKKIAPETRISI-----EVLNERICIQVGS---QCSTNESEKPSILV 114
 QY 125 ETTYWIS-PQGITETKVQDMDCVYNNQYLCSMKPGIGVLLDTNLYNLFYWEGLDHALQ 183
 DB 115 EKC--ISPPEGDPESAVTELOCIWHNLSYMKCSWLPGRNTSPDNTLYLYWHSLEKIHQ 172
 QY 184 CVDYKADQGNIGRFPYLEASD--YKDFYICVNGSSSENKPIRSYFTFQIQNTVVKPLPP 241
 DB 173 C-ENIFREGQYFGCSFDLTQVKDSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP 231
 QY 242 --VLTFTRESSCEIKLWSITPLGIPARCFDYEIEIEDDTT-----LVTATVENETY 293
 DB 232 HIKNLSFHND--DLYVQWENPQNF-I-SRCLFYEVYVNSQSTETHNVFYVQAEKCNPEF 287
 QY 294 TLKNTNTRQLCFVY-----RSKVNIVC--SDGIWSEWSDKQCEWGEDLSKK 339
 DB 288 ERNVNTS---CFMVGVLPTLTNTVIRVTKNLCLYEDDKLWSNQEM-----SIGKK 339
 QY 340 TLLRFWLPP-----GFTLLIVFTVGL--LLRKNPTYP-KMIEFFEDF 379
 DB 340 RNSTLYTMLLIVPVIVAGAILVLLYLLKRLKIIFPPIDPDPGKIFKEMFGD 391
 RESULT 5
 ID PRLR_CHICK STANDARD; PRT; 831 AA.
 AC Q04594;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPRLP).
 GN PRLR.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEHORN; TISSUE-Kidney;
 RX MEDLINE-93075121; PubMed-1445292;
 RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
 RT "Double antenna structure of chicken prolactin receptor deduced from
 the cDNA sequence.";
 RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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DR ENBL; D13154; BAA02439.1; -. CC
DR PIR; JQ1655; JQ1655. CC
DR HSP; PI6471; IBP3. CC
DR InterPro; IPR000950; -. CC
DR InterPro; IPR001777; -. CC
DR InterPro; IPR002465; -. CC
DR Pfam; PF00041; fn3; 4. CC
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1. CC
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat. CC
FT SIGNAL 1 FT CC
FT CHAIN 24 831 PROLACTIN RECEPTOR. CC
FT FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL). CC
FT TRANSMEM 439 459 POTENTIAL. CC
FT FT DOMAIN 460 831 CYTOPLASMIC CC
FT FT DOMAIN 25 122 FIBONECTIN TYPE-III. CC
FT FT DOMAIN 123 225 FIBONECTIN TYPE-III. CC
FT FT DOMAIN 228 325 FIBONECTIN TYPE-III. CC
FT FT DOMAIN 326 428 FIBONECTIN TYPE-III. CC
FT DISULFID 36 46 BY SIMILARITY. CC
FT FT DISULFID 75 86 BY SIMILARITY. CC
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL). CC
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL). CC
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL). CC
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL). CC
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL). CC
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL). CC
FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL). CC
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL). CC
FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL). CC
SQ SEQUENCE 831 AA; 994102 MW; 1C4E75791DCADB9 CRC64;
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RESULT 7
PRLR_MELGA STANDARD; PRT; 831 AA.
ID PRLR_MELGA STANDARD; PRT; 831 AA.
AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).
GN PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxId=9103;
RN [1]
RN SEQUENCE FROM N.A.
RP
RT TISSUE=Kidney;
RX MEDLINE=97057891; PubMed=8902221;
RA Zhou J.F., Zadowrny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo."
RT Biol. Reprod. 55:1081-1090(1996).
RN [2]
RN SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RP
RT TISSUE=Ovary;
RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
RC Submitted (MAR-1995) to the EMBL/GenBank/DDAJ databases.
RL
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC
CC -----
CC EMBL; L76587; AAB01544.1; -
CC DR DR
CC EMBL; U22947; AAA75038.1; -
CC DR DR
CC EMBL; U22924; AAA75039.1; -
CC DR DR
CC HSP; P16471; LBP3.
CC
CC InterPro: IPR000950; -
CC DR DR
CC InterPro: IPR001777; -
CC DR DR
CC InterPro: IPR002465; -
CC DR DR
CC Pfam: PF00041; fn3; 4.
CC DR DR
CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
CC DR DR
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
CC KW
CC SIGNAL 1 23
CC FT CHAIN 24 831
CC DR DR
CC DOMAIN 24 438
CC FT FT
CC TRANSMEM 439 459
CC FT FT
CC DOMAIN 460 831
CC DR DR
CC DOMAIN 25 122
CC FT FT
CC DOMAIN 123 225
CC FT FT
CC DOMAIN 228 325
CC FT FT
CC FIBRONECTIN TYPE-III.
CC FIBRONECTIN TYPE-III.

```

RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;
 RT "Characterization of the human interleukin-2 receptor gamma chain
 gene.";
 RL J. Biol. Chem. 268:13601-13608(1993).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.
 RX MEDLINE=94004847; PubMed=8401490;
 RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,
 RA Willard H., Henthorn P.S.;
 RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated
 RT in X-linked severe combined immunodeficiency, SCID_{HL}.";
 RL Hum. Mol. Genet. 2:1099-1104(1993).
 RN [4]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE=94090315; PubMed=8266076;
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
 RA Arai K.-I., Sugamura K.;
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
 RT receptors for IL-2 and IL-4.";
 RL Science 262:1874-1877(1993).
 RN [5]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE=94090317; PubMed=8266078;
 RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,
 RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-4 receptor.";
 RL Science 262:1880-1883(1993).
 RN [6]
 RP IDENTIFICATION AS A IL-7R SUBUNIT.
 RX MEDLINE=94090316; PubMed=8266077;
 RA Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-7 receptor.";
 RL Science 262:1877-1880(1993).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamrough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling.";
 RL Structure 2:839-851(1994).
 RN [8]
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE=94130970; PubMed=8299698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 RA de Saint Basile G.;
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 RT severe combined immunodeficiency disease result in the loss of
 RT high-affinity IL-2 receptor binding.";
 RL Eur. J. Immunol. 24:475-479(1994).
 RN [9]
 RP VARIANT XSCID LYS-68.
 RX MEDLINE=94375038; PubMed=8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 RT the interleukin-2 receptor gamma chain gene in SCID_{HL} that
 RT differentially affect the mRNA processing.";
 RL Genomics 21:291-293(1994).
 RN [10]
 RP VARIANT XSCID HIS-162.
 RX MEDLINE=94300093; PubMed=8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 RT receptor gamma-chains in patients with X-linked severe combined
 RT immunodeficiency.";
 RL J. Immunol. 153:1310-1317(1994).
 RN [11]
 RP VARIANT XSCID ASN-39.

RX MEDLINE=95023932; PubMed=7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 RT chromosome-linked severe combined immunodeficiency with peripheral T
 RT cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
 RN [12]
 RP VARIANTS XSCID CYS-226 AND HIS-226.
 RX MEDLINE=95397841; PubMed=7668284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 RT gene causing human X-linked severe combined immunodeficiency.";
 RL Am. J. Hum. Genet. 57:564-571(1995).
 RN [13]
 RP VARIANT XSCID SER-183.
 RX MEDLINE=96013903; PubMed=7557965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 RA Levinsky R.L., Kinnon C.;
 RT "Screening for mutations causing X-linked severe combined
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand
 RT conformation polymorphism analysis.";
 RL Hum. Genet. 96:427-432(1995).
 RN [14]
 RP VARIANT XSCID GLN-237 G-H-W INS.
 RX MEDLINE=95164726; PubMed=7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 RT gamma-chain mutation causing X-linked severe combined
 RT immunodeficiency.";
 RL J. Clin. Invest. 95:895-899(1995).
 RN [15]
 RP VARIANT XSCID GLN-271.
 RX MEDLINE=95190013; PubMed=7883965;
 RA Schmalstieg F.C., Leonard W.J., Noguchi M., Berg M., Rudloff H.E.,
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 RT moderate form of X-linked combined immunodeficiency.";
 RL J. Clin. Invest. 95:1169-1173(1995).
 RN [16]
 RP VARIANT XSCID ARG-115.
 RX MEDLINE=97042245; PubMed=8900089;
 RA Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B.,
 RA Mueller-Fleckenstein I., Horneff G., Schroten H., Fischer A.,
 RA de Saint Basile G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 RT spontaneous reversion of the genetic defect in T cells.";
 RL New Engl. J. Med. 335:1563-1567(1996).
 RN [17]
 RP VARIANT XSCID GLN-285.
 RX MEDLINE=97295088; PubMed=9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 RA Cant A., Kinnon C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 RT common gamma chain mutation.";
 RL Hum. Genet. 99:677-680(1997).
 RN [18]
 RP VARIANT XSCID CYS-222.
 RX MEDLINE=98064061; PubMed=9399950;
 RA Sharfe N., Shahar M., Roifman C.M.;
 RA "An interleukin-2 receptor gamma chain mutation with normal thymus
 RT morphology.";
 RL J. Clin. Invest. 100:3036-3043(1997).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
 CC IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMAGLOBULINEMIA, SWISS TYPE
 CC OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD132 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd132.htm".
CC -!- DATABASE: NAME=IL2Rbase; NOTE=X-linked SCID mutation database;
CC WWW="http://www.nhri.nih.gov/DIR/GMBB/SCID/".
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CC -----
DR EMBL; D11086; BAA01857.1; -.
DR EMBL; L12183; AAA59145.1; -.
DR EMBL; L12178; AAA59145.1; JOINED.
DR EMBL; L12176; AAA59145.1; JOINED.
DR EMBL; L12177; AAA59145.1; JOINED.
DR EMBL; L12179; AAA59145.1; JOINED.
DR EMBL; L12180; AAA59145.1; JOINED.
DR EMBL; L12181; AAA59145.1; JOINED.
DR EMBL; L12182; AAA59145.1; JOINED.
DR EMBL; L19546; AAC37524.1; -.
DR PIR; A42565; A42565.
DR PDB; 1ILM; 26-JAN-95.
DR PDB; 1ILN; 26-JAN-95.
DR MIM; 308380; -.
DR MIM; 300400; -.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
Query Match 10.5%; Score 220; DB 1; Length 369;
Best Local Similarity 25.5%; Pred. No. 8.1e-11;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;
Qy 97 LNKGEAKIHTLLPQCCTNGSE-VOSSWAETTYWISPOGIPETKVDMDCVYNNQWYLLC 155
Db 19 LGVGLNTTILR-----PNGNEDTADFLTMTDLSLSTVTLPLPEVQCFVFNVEYMC 72
Qy 156 SW-----KPGIGVLLDNYNLFYWEGLDR--ALQVDYIKADGQNTGCRFPYLEASDY 207
Db 73 TWNSSEPOQ-----TNLTLHWYKNSDNDKVKQCSHYLFSEITSGCQLQKKEHLY 125
Qy 208 KDFYICVNGSSNKPISRYTFQLONLVKKLPVPVYLTFTRESSCEIKLKWISPLGPIPA 267
Db 126 QTFVVQLQDPRE--PRQATQMLKLQNLVIFWAPENLTLHLKLSQLELWN---NRFLN 180
Qy 268 RCFDYEIFEIRD-DTTLVTATVE-NETYLTKTNTETQLCFVVRKSVNIYCSDDGIWSEW 325
Db 181 HCLEHLVQYRTDWDHSWTEQSDYVRHKFSLPSVDGQKRYTRVRSRNPGLCSAQHSEW 240
Qy 326 SDKQCWEGEDLSKTLIRFWLPFGFILLIVIFVVG 360
Db 241 SHPIHW-GSNTSKEN-----PFLFALEAVVISVG 268
RESULT 9
PRLR_COLLI
ID PRLR_COLLI STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cropsac;

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RX MEDLINE=94283267; Pubmed=7516866;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin
RT receptor.";
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL; U07694; AAA20646.1; -.
DR HSP; P16471; Ibp3.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT DOMAIN 461 830
FT DOMAIN 25 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
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FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
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FT CARBOHYD 830 AA; 94507 MW; 38074E83CDF69EFF CRC64;
SQ SEQUENCE
Query Match 10.3%; Score 216.5; DB 1; Length 830;
Best Local Similarity 24.4%; Pred. No. 4.2e-10;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;
Qy 18 TFGCTSSDTEIKVNPDPQDFEIVDPGLG-----DPOYVDVTSVQDPAPVNLSETKTSASTYLLAKW 150
Db 97 TTYNITVAMNEIGSNSS-----DPOYVDVTSVQDPAPVNLSETKTSASTYLLAKW 150
Qy 54 QPPLSLDFHRECTV-EYELKYRNIGSETWTKITIKNLHYKDFLNGKIEAKIHTLPLWQ 112
Db 151 SPPPLADVTNSHYRYELRLKPEKEWETV---SVGVQYQYKVNRLQAGVYVVOVR 206
Qy 113 CTNGSEVQSSWAETTYWISPOG-IPETKVDQMDCVYNNQWYLLCSWKPGLVDLTNNL 171
Db 207 CVLDIGSEWSSSERHIHPNGESFPPEKPTTIKRSPEKEFTTCWNKPGSGGHTNYTL 266
Qy 172 FYWVEGLDHALQVDYIKADGQNTGCRFPYLEASDYKDFYICVNGSSNKPISRYTFQ 231
Db 267 LYSKEGEVERVECPDY-KTAGPN-SCYFDKKHTSFYTYNITVKATNEIGSNVSDPLYVD 324
Qy 232 LQNLVKKLPVYLTFTRESSCEIK-----LKWIS-PLGPIPA--RCFDYEIFEIRDDTTLV 284
Db 325 VTYIVQTDPPVNVTLKLTVNRRKPYLVLTWSPPLADVRSGLTLDYELRLKPEEA--- 381

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QY 285 TATVENETTLKTTNETRQLCFVY-----RSKVNIVCSD--GIWSEWS-DKOCWEGEDLS 337
 Db 382 -----EWETIFVQOQTHYKMFSLNPKKIVQIHCKPDHGSWSLSLEYLIQIPDFR 436
 QY 338 KKTLLRFLWPGFILLIVFV 358
 Db 437 IKDMV-VMIIVGLSSILCLV 456

RESULT 10
 CYRG_MOUSE STANDARD; PRT; 369 AA.
 AC P34902;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
 GN (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93277575; PubMed=8503926;
 RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
 RT "Cloning of the mouse interleukin 2 receptor gamma chain:
 RT demonstration of functional differences between the mouse and human
 RT receptors";
 RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CBA/CA;
 RA MEDLINE=93391374; PubMed=8378320;
 RA Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
 RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
 RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
 RT IL-2R gamma chain expression";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93366191; PubMed=8359699;
 RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
 RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
 RT gamma";
 RL Gene 130:303-304(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95104285; PubMed=7805729;
 RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
 RA Fischer A., de Saint Basile G.;
 RT "The murine interleukin-2 receptor gamma chain gene: organization,
 RT chromosomal localization and expression in the adult thymus.";
 RL Eur. J. Immunol. 24:3014-3018(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX STRAIN=B6.S;
 RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
 RA Dougherty G.J.;
 RT "Molecular mechanisms regulating the hyaluronan binding activity of
 RT the adhesion protein CD44";
 RL J. Neurocol. 26:231-239(1995).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D13821; BAA02974.1; -
 DR EMBL; U21795; AAA64279.1; -
 DR EMBL; D13565; BAA02760.1; -
 DR EMBL; L20048; AAA39286.1; -
 DR EMBL; S75852; AAB32904.1; -
 DR EMBL; S75844; AAB32904.1; JOINED.
 DR EMBL; S75845; AAB32904.1; JOINED.
 DR EMBL; S75847; AAB32904.1; JOINED.
 DR EMBL; S75848; AAB32904.1; JOINED.
 DR EMBL; S75849; AAB32904.1; JOINED.
 DR EMBL; S75850; AAB32904.1; JOINED.
 DR EMBL; S75851; AAB32904.1; JOINED.
 DR EMBL; X75337; CAA53085.1; -
 DR PIR; JN0592; JN0592.
 DR PIR; JN0775; JN0775.
 DR HSP; P31785; IILN.
 DR MGD; MGI:96551; IL2rg.
 DR InterPro; IPR000950; -
 DR InterPro; IPR001777; -
 DR InterPro; IPR002465; -
 DR Pfam; PF00041; fn3; 1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 369
 FT DOMAIN 23 263
 FT TRANSSEM 264 284
 FT DOMAIN 285 369
 FT DISULFID 62 72
 FT CARBOHYD 102 115
 FT CARBOHYD 71 71
 FT CARBOHYD 75 75
 FT CARBOHYD 84 84
 FT CARBOHYD 96 96
 FT CARBOHYD 159 159
 FT CARBOHYD 164 164
 SQ SEQUENCE 369 AA; 42241 MW; CB2DSAB459077AC7 CRC64;
 Query Match 10.1%; Score 212.5; DB 1; Length 369;
 Best Local Similarity 26.9%; Pred. No. 3.3e-10;
 Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;
 QY 136 PETKVQDMCVYNNQYLLCSW----KPGIGVLDNTNLYWYEGLDHAL--QCVDYIK 189
 Db 53 PTLPLPEVQCFVFNIEVMNCTWSSEPA-----TNLTHRYKVSNDNTFQCCHYLF 107
 QY 190 ADGQNICGRFFYLEADYKDFYICVNGSSSENKPIRSSYFTFQLQNIYKPLPPVLTFTRE 249
 Db 108 SKETSGCQIQEKEDIQLYQTFVQL--ODPKORRAVQKLNQLNQLVPRAPENLTLSNL 165
 QY 250 SSCBIKLKWSIPGLPIPARCFDYIEIREDD--DTTLVTATVENE--TYTLKTTNETRQLCFV 307
 Db 166 SESQLELRWK--SRHIKERCQLYLVQYRSNDRSWTELIVNHEPRFSLPSVDLKRKYTR 223
 QY 308 VRSKVNYCSDGDTWSEWSKQCWEG-----EDLSKKTLRLFWLPGF--ILILVFTVGL 361
 Db 224 VRSYNPICGSSQQSKWSQPVHMGSHTEENPSLFALEAVLPVGTMLTITLIFVYCW 283
 QY 362 LLRKPNYP 370
 Db 284 LERMPPIPP 292

RESULT 11
CYRG_CANFA STANDARD; PRT; 373 AA.
AC P40321; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=95130114; PubMed=7829104;
RA Henthorn P.S.; Somberg R.L.; Fimiani V.M.; Puck J.M.; Patterson D.F.;
RA Felsburg P.J.;
RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
severe combined immunodeficiency is a homologue of the human
disease.";
RT disease.";
RL Genomics 23:69-74(1994).
CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
INTERLEUKINS.
CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
PROBABLY ALSO THE IL-13 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
SEVERE COMBINED IMMUNODEFICIENCY.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; U04361; AAC48403.1; -
CC HSP; P31785; IILN.
CC InterPro: IPR000950; -
CC InterPro: IPR001777; -
CC InterPro: IPR002465; -
CC Pfam; PF00041; fn3; 1.
CC PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 373 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 261 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 262 283 POTENTIAL.
FT DOMAIN 284 373 CYTOSOLASMIC (POTENTIAL).
FT DOMAIN 151 249 FIBRONECTIN TYPE-III.
FT DISULFID 62 72 POTENTIAL.
FT DISULFID 102 115 POTENTIAL.
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42516 MW; 03A0DE1F8B089D8B CRC64;
Query Match 9.9%; Score 208; DB 1; Length 373;
Best Local Similarity 26.0%; Pred. No. 7.9e-10;
Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;
QY 115 NGSE-----VQSSWAETTYWISPGQIPETKVQDMDCVYNNQYLLCSW-----KPGI 161

Db 31 NGNEDITPDEFIATPSET---LSVSLPLPEVQ---CFVFNVEYMNCTWNSSEPR-- 82
QY 162 GVLLDTNINLFYWEGL--DHALQCVDIYIKADGNICRCPPYLEASDYKDFYICVNGSSE 219
Db 83 -----TNLTLYWYKNSNDKVOECGHLYFSREVTTAGCKEELHLYETFFVQLRDPRE 137
QY 220 NKPIRSSYFTFOQNIYKPLPPVYLTFTRESSCEIKLKWSPILGPPIPARCFDYEIREDR 279
Db 138 --PRRQSTQKQLQNLVWPAPENLTLHNSOLELSWS---NRHLDHCLHEHVQVVRSD 192
QY 280 -DTTLVTATVEN-ETYLTKTNTTCQFVVRSKVNIYCSDDGIWSEWSKQWEGEDLS 337
Db 193 WDRSWTEQSVDRHSFSLPSVDGQKFFYFRVRSRNPCLGSAQRWSEWSPIHW-GSNTS 251
QY 338 KTYLL-----RFWLPFGFILLIVFV 358
Db 252 KENPLFAEAVLPLGSMGLIISLI 276
RESULT 12
IL3B_MOUSE STANDARD; PRT; 878 AA.
AC P26934;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR CLASS II BETA CHAIN PRECURSOR (COLONY
STIMULATING FACTOR 2 RECEPTOR, BETA 2 CHAIN).
GN CSF2RB2 OR A12CA OR IL3RB2 OR IL3R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90117145; PubMed=2404337;
RA Itoh N., Yonehara S., Schreurs J., Gorman D.M., Maruyama K., Ishii A.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning of an interleukin-3 receptor gene: a member of a distinct
receptor gene family.";
RL Science 247:324-327(1990).
CC -!- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3
RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE
OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5
AND GM-CSF RECEPTORS.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; M29855; AAA39295.1; -
CC PIR; A40091; A40091.
CC MGD; MGI:1339760; Csf2rb2.
CC InterPro; IPR000950; -
CC InterPro; IPR001777; -
CC InterPro; IPR002465; -
CC Pfam; PF00041; fn3; 2.
CC PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 878 INTERLEUKIN-3 RECEPTOR CLASS II BETA
CHAIN.
FT DOMAIN 23 440 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 441 462 POTENTIAL.
FT DOMAIN 463 878 CYTOSOLASMIC (POTENTIAL).

Qy 49 LYLOWPPL---SLDHKECTVEYELKYRNISETWKTIIITKN-----LHYKDGFDLNGK 100
Db 151 FLEWSVLGDAQYSLSSKDIEFEVAYKRL-QDSWEDAYSILHTSKFOVNEPKLFLPNS 209
Qy 101 IEA-KIHT-LLPWQCTNGSEVQSSWAETTYWISPOGIPETKVDMDCVYINWOYLLCSWK 158
Db 210 IYAPRVTRLYPGSSLSGR--PSRMSPEAHWDSOPG-DKAQPQNLQCFDGIQSLHCSWE 266
Qy 159 PGIGVLLDTNLYWYVEGLDHALQCVDIK-ADQONI---GCRFPYLEASDYKDFVIC 213
Db 267 VMTQTGVSFGLYRPSVPAPEKCSPPVKEPPGASVYTRYHCSLPVPEPSAHSQYTVS 326
Qy 214 VNGSENKPIRSSYFTFOLQNIIVPLPPVYLTFTRSSCEIKLKSIPGLPIPARCFDYE 273
Db 327 V-----KHLEQGGKFINSYNHIQMEPTLNLTKNRDS---YSLHWETQKMAYSFIEHTFQ 377
Qy 274 IEIREDDTTLTAIVEN--ETYTLKTTNETQLCFVVRKSNYIYCSDDGIWSEHSDKOCW 331
Db 378 VOYKKKSDSWEDSKTENLDRAHSMDLSOLEPDTSYCARVRVKPISNYDGIWSEYTW 437
Qy 332 EGEDLSKKTLLRFLWLPFGFILILVIFVTGLLL 363
Db 438 K-TDWVWPTL---WI-----VLILVFLILTL 461

Search completed: September 1, 2001, 19:16:24
Job time: 506 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:05:53 ; Search time 35.33 Seconds
(without alignments)
221.464 Million cell updates/sec

Title: US-09-077-817-2

Perfect score: 2104

Sequence: 1 MAFVCLAIGCLYTLFTLSTTF.....LLLRKPNTPKMIPEFFCDT 380

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCFUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2104	100.0	380	1	US-08-609-572-4
2	2104	100.0	380	4	US-08-841-751-4
3	2104	100.0	380	4	US-08-846-340-4
4	1194.5	56.8	383	1	US-08-609-572-2
5	1194.5	56.8	383	4	US-08-841-751-2
6	1194.5	56.8	383	4	US-08-846-340-2
7	311.5	14.8	420	1	US-07-757-390-13
8	311.5	14.8	420	1	US-08-442-282-13
9	311.5	14.8	420	1	US-08-442-281-13
10	311.5	14.8	420	2	US-08-939-727-13
11	310.5	14.8	396	1	US-07-757-390-14
12	310.5	14.8	396	1	US-08-442-282-14
13	310.5	14.8	396	1	US-08-442-281-14
14	310.5	14.8	396	2	US-08-939-727-14
15	295.5	14.0	427	4	US-08-969-125-9
16	293	13.9	313	3	US-08-836-561-106
17	292	13.9	335	1	US-07-947-130-2
18	292	13.9	335	1	US-08-421-822-2
19	292	13.9	335	1	US-08-421-823-2
20	247	11.7	398	1	US-07-757-390-6
21	247	11.7	398	1	US-08-442-282-6
22	247	11.7	398	1	US-08-442-281-6
23	247	11.7	398	2	US-08-939-727-6
24	247	11.7	415	1	US-07-757-390-5
25	247	11.7	415	1	US-08-442-282-5
26	247	11.7	415	1	US-08-442-281-5
27	247	11.7	415	2	US-08-939-727-5

Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 69, Appli
Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-609-572-4
; Sequence 4, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-609-572-4

Query Match 100.0%; Score 2104; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 4.2e+208;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTLSTTFCTSSDTEIKVNPQDFEIVDPGLVLYLQWQPLSLD 60

Db 1 MAFVCLAIGCLYTLSTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNKGEAKIHLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNKGEAKIHLLPWOCTNGSEVQ 120
Qy 121 SSWAETTWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDNTNLYFYWEGLDH 180
Db 121 SSWAETTWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDNTNLYFYWEGLDH 180
Qy 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Qy 241 PVLFTFTRESSCEIKLWISIPGLPIPARCFDYEIEIREDDTTLVATVAVENETYLKTTNE 300
Db 241 PVLFTFTRESSCEIKLWISIPGLPIPARCFDYEIEIREDDTTLVATVAVENETYLKTTNE 300
Qy 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGDLSSKTLRLFWLPGFLLILVIFVTG 360
Db 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGDLSSKTLRLFWLPGFLLILVIFVTG 360
Qy 361 LLLRKPNTYPRKMIPEFFCDT 380
Db 361 LLLRKPNTYPRKMIPEFFCDT 380

RESULT 2

US-08-841-751-4
; Sequence 4, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-841-751-4
Query Match 100.0%; Score 2104; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 4.2e-208;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFVCLAIGCLYTLSTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
Db 1 MAFVCLAIGCLYTLSTTFCGCTSSDTEIKVNPQDFEIVDPGVLGYLQWQPPLSLD 60
Qy 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNKGEAKIHLLPWOCTNGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNKGEAKIHLLPWOCTNGSEVQ 120
Qy 121 SSWAETTWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDNTNLYFYWEGLDH 180
Db 121 SSWAETTWISPOGIPETKVQDMDCVYNNWQYLLCSKPKGIGVLLDNTNLYFYWEGLDH 180
Qy 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Db 181 ALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
Qy 241 PVLFTFTRESSCEIKLWISIPGLPIPARCFDYEIEIREDDTTLVATVAVENETYLKTTNE 300
Db 241 PVLFTFTRESSCEIKLWISIPGLPIPARCFDYEIEIREDDTTLVATVAVENETYLKTTNE 300
Qy 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGDLSSKTLRLFWLPGFLLILVIFVTG 360
Db 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGDLSSKTLRLFWLPGFLLILVIFVTG 360
Qy 361 LLLRKPNTYPRKMIPEFFCDT 380
Db 361 LLLRKPNTYPRKMIPEFFCDT 380

RESULT 3

US-08-846-340-4
; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-4

Query Match 100.0%; Score 2104; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 4.2e-208;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTSTFGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPPLSLD 60
DB 1 MAFVCLAIGCLYTLFTSTFGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPPLSLD 60
QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
DB 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
QY 121 SSWAETTYWISPOGIPETKVODMDCVYNNWQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
DB 121 SSWAETTYWISPOGIPETKVODMDCVYNNWQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
QY 181 ALOQVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIKPLP 240
DB 181 ALOQVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIKPLP 240
QY 241 PVYLTFRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLTAVENETYLTKTTNE 300
DB 241 PVYLTFRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLTAVENETYLTKTTNE 300
QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQWEGEDLSKTLRLRFLWLPFGFTLLILVIFVTG 360
DB 301 TRQLCFVVRKVNICYSDGDIWSEWSKQWEGEDLSKTLRLRFLWLPFGFTLLILVIFVTG 360
QY 361 LLRLKPNTPYKMIPEFFCDT 380
DB 361 LLRLKPNTPYKMIPEFFCDT 380

RESULT 4
US-08-609-572-2
Sequence 2, Application US/08609572
Patent No. 5710023
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,572
FILING DATE:
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-572-2

Query Match 56.8%; Score 1194.5; DB 1; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.4e-114;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
QY 1 MAFVCLAIGCLYTLFTSTFGCTSSDTEIKVNPQDFEIVDPGVLGYLYLOWPPPLSLD 60
DB 1 MAFV--HRCCLFLLCTITGYS----LEIKVNPQDFEILDGCLLGYLYLOWAPPVVIE 54
QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
DB 55 KFKGCTLEYELKYRNVDSDSWKTIITRNLYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114
QY 121 SSWAETTYWISPOGIPETKVODMDCVYNNWQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
DB 115 SPWTEASYGISDEGSLETKIQDMKCIYNNWQYLLCSWKPGKTVSDNTYTMFWYEGLDH 174
QY 181 ALOQVDYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNIKPLP 240
DB 175 ALOQADYIHDQNRKNGVCLNLDSSDYKDFYICVNGSKLEPIRSSYFTFOLQNIKPLP 234
QY 241 PVYLTFRESSECEIKLWSIPLGPIPARCFDYEIEIREDDTTLTAVENETYLTKTTNE 300
DB 235 PEFLLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVREDDISWESATDKNDMKLRANE 294
QY 301 TRQLCFVVRKVNICYSDGDIWSEWSKQWEGEDLSKTLRLRFLWLPFGFTLLILVIFVTG 360
DB 295 SEDLCFFVRCKVNIYCADGDIWSEWSEECWEGYTGTPDPSKII-FIVPVCFLFFFLLLLLC 353
QY 361 LLRLKPNTPYKMIPEFFCDT 372
DB 354 LIVEKEPEPTL 365

RESULT 5
US-08-841-751-2
Sequence 2, Application US/08841751
Patent No. 6214559
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/841,751

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/609,572

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 383 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-841-751-2

Query Match 56.8%; Score 1194.5; DB 4; Length 383;

Best Local Similarity 58.9%; Pred. No. 1.4e-114;

Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLAIGCLYTLSTTFCGTSSTDEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60

DB 1 MAFV--HIRCLCFILLCITIGYS----LEIKVNPQDFEILDGGLGLGYLYLQWPPPVVIE 54

QY 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120

DB 55 KFKGCTLEYELKYNVDSDSWKTIITRNLIYKDGFDLNGKIEGKIRTHLSHCCTNGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180

DB 115 SPWIEASYGIDSEGSLETKIQDMKCIYNNQYLLCSWKPGKTVSDNYTMFFWYEGLDH 174

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240

DB 175 ALQCADYLQHDENKVGCKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTVFOLQNIKPLP 234

QY 241 PVYLTFRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLTATVENETYLKTTNE 300

DB 235 PEFLLHSVENSIDIRMKWSTPGGPPIPRCYTYEIVIREDDISWESATDKNDKMLKRRANE 294

QY 301 TROLCFVVRKVNICYSDGDIWSEWSKQWEGEDLSKTKTLRLFWLPFGFILLIVFVTG 360

DB 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEGYTGPDISKII-FIVPVCLEFFIFLLLLLC 353

QY 361 LLLRKPNTYPKM 372

DB 354 LIVEKEPEPTL 365

RESULT 6

US-08-846-340-2

Sequence 2, Application US/08846340

Patent No. 6248714

GENERAL INFORMATION:

APPLICANT: Collins, Mary

APPLICANT: Donaldson, Debra

APPLICANT: Fitz, Lori

APPLICANT: Neben, Tamlyn

APPLICANT: Whitters, Matthew

APPLICANT: Wood, Clive

TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-2

Query Match 56.8%; Score 1194.5; DB 4; Length 383;

Best Local Similarity 58.9%; Pred. No. 1.4e-114;

Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLAIGCLYTLSTTFCGTSSTDEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60

DB 1 MAFV--HIRCLCFILLCITIGYS----LEIKVNPQDFEILDGGLGLGYLYLQWPPPVVIE 54

QY 61 HFKECTVEYELKYNIGSETWKTITITKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120

DB 55 KFKGCTLEYELKYNVDSDSWKTIITRNLIYKDGFDLNGKIEGKIRTHLSHCCTNGSEVQ 114

QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180

DB 115 SPWIEASYGIDSEGSLETKIQDMKCIYNNQYLLCSWKPGKTVSDNYTMFFWYEGLDH 174

QY 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNIKPLP 240

DB 175 ALQCADYLQHDENKVGCKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTVFOLQNIKPLP 234

QY 241 PVYLTFRESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLTATVENETYLKTTNE 300

DB 235 PEFLLHSVENSIDIRMKWSTPGGPPIPRCYTYEIVIREDDISWESATDKNDKMLKRRANE 294

QY 301 TROLCFVVRKVNICYSDGDIWSEWSKQWEGEDLSKTKTLRLFWLPFGFILLIVFVTG 360

DB 295 SEDLCFFVRCKVNIYCADDGIWSEWSEECWEGYTGPDISKII-FIVPVCLEFFIFLLLLLC 353

QY 361 LLLRKPNTYPKM 372

DB 354 LIVEKEPEPTL 365

RESULT 7

US-07-757-390-13

Sequence 13, Application US/07757390

Patent No. 5453491

GENERAL INFORMATION:

APPLICANT: Takatsu, Kiyoshi

APPLICANT: Tomimaga, Akira

APPLICANT: Takagi, Satoshi

APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,390
FILING DATE: 19910910
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-757-390-13

Query Match 14.8%; Score 311.5; DB 1; Length 420;
Best Local Similarity 26.9%; Pred. No. 1e-23;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

Qy 27 DTEIKVNPQDFEIVDPGILGYLQWPPPLSLDFHFKRECTVEYELKYNIGSETWKTIIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82

Qy 87 KNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVSSWAETTYWISPOGIPETKVODMDCV 146
Db 83 ES---KCVTLHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSGTGVNLTCT 135

Qy 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF---WYEGDLHALQCYDYIKAD 191
Db 136 TTTTNDYSLRSYQVSLHCTWLVGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189

Qy 192 -QONIGCRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
Db 190 LGRNIACWFFRTFLSKGRDLAVLVNGSSKHSARFPDQLFALHAIDQINPLNVAEI 249

Qy 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVATVENETTYLTKTNETQLCFV 308
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIKHNTRNGYLQIEKLTNAFISIIDLSKYDVQV 308

Qy 309 RSKYNIYCSDDGIWSESDKOCWEGEDLSKTLRLFWLPFGFILIL-----VIFVTGLL 362
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATCIFILLISLI 361

Qy 363 LRKNTTPKMP 374
Db 362 CKICHLWIKLFP 373

RESULT 8
US-08-442-282-13
; Sequence 13, Application US/08442282

Patent No. 5760204
GENERAL INFORMATION:
APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tomioka, Akira
APPLICANT: Takagi, Satoshi
APPLICANT: Murata, Yoshiyuki
TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,282
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/757,390
FILING DATE: 10-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-442-282-13

Query Match 14.8%; Score 311.5; DB 1; Length 420;
Best Local Similarity 26.9%; Pred. No. 1e-23;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

Qy 27 DTEIKVNPQDFEIVDPGILGYLQWPPPLSLDFHFKRECTVEYELKYNIGSETWKTIIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82

Qy 87 KNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVSSWAETTYWISPOGIPETKVODMDCV 146
Db 83 ES---KCVTLHKGFSAVRILQ---NDHSLASSWASAEHL-APPGSGTGVNLTCT 135

Qy 147 -----YNNQYLL-CSWKPGIGVLLDTNLYF---WYEGDLHALQCYDYIKAD 191
Db 136 TTTTNDYSLRSYQVSLHCTWLVGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189

Qy 192 -QONIGCRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVYLFTFR 248
Db 190 LGRNIACWFFRTFLSKGRDLAVLVNGSSKHSARFPDQLFALHAIDQINPLNVAEI 249

Qy 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVATVENETTYLTKTNETQLCFV 308
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIKHNTRNGYLQIEKLTNAFISIIDLSKYDVQV 308

Qy 309 RSKYNIYCSDDGIWSESDKOCWEGEDLSKTLRLFWLPFGFILIL-----VIFVTGLL 362
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATCIFILLISLI 361


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Qy 147 -----YNNQYLL-CSWKPQIGVLLDTNRYLFY-----WYGLDHALQCVDYIKAD 191
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 136 TTTEDNTSRLRSYQVSLHCTWLVGTDAPEDTQVFLYRYGSWTE-----ECQYSKDT 189
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFOLQNIYKPLPPVYLTFTFR 248
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 190 LGRNIACTPRTFILSKGRDMLAVLVNGSSKHSARPPDQLFALHAIDQINPPLNVTAEI 249
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 249 ESSCEIKLWSPIGLPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNETROLCFWV 308
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 250 EGT-RLSIQWEKPSVAFPIHCFDYEKTHNTRNGVLOIEKLTNAFISIIDLSKYDVQV 308
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 309 RSKVNIYSDGDIWSEWSDKOCWEGEDLSKTLRFLWLPFGFILL-----VIFVTGLL 362
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 309 RAAVSSMCREAGLSEWS-QPIYVGNDEHKP--LREW----FVIVIMATIFILLISLI 361
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 363 LRKPNTYKMP 374
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 362 CKICHLWIKLFP 373
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |

RESULT 11
US-07-757-390-14
; Sequence 14, Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-757-390-14

Query Match 14.8%; Score 310.5; DB 1; Length 396;
-Best Local Similarity 26.6%; Pred. No. 1.2e-23;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

Qy 27 DFEIKVNPQDFEIVDPGYLYLQWOPPLSLDFHFKECTVEYELKYRNIGSETWTKTIT 86
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 25 DEKISLLPPVNTIKVTG-LAQVLLQWPNPDQEQ-RNVNLEYQVKINAPKEDDYETRI 82
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
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Qy 87 KNLHYKGFEDLNKGTEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 83 ES---KCVTILHKFSASVRILO---NDHSLLASSWASAEHL-APPGSPGTSIVNLACT 135
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 147 -----YNNQYLL-CSWKPQIGVLLDTNRYLFY-----WYGLDHALQCVDYIKAD 191
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 136 TTTEDNTSRLRSYQVSLHCTWLVGTDAPEDTQVFLYRYGSWTE-----ECQYSKDT 189
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFOLQNIYKPLPPVYLTFTFR 248
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 190 LGRNIACTPRTFILSKGRDMLAVLVNGSSKHSARPPDQLFALHAIDQINPPLNVTAEI 249
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 249 ESSCEIKLWSPIGLPIPARCFDYEIEIREDDTTLVTATVENETYLKTTNETROLCFWV 308
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 250 EGT-RLSIQWEKPSVAFPIHCFDYEKTHNTRNGVLOIEKLTNAFISIIDLSKYDVQV 308
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 309 RSKVNIYSDGDIWSEWSDKOCWEGEDLSKTLRFLWLPFGFILL-----VIFVTGLL 362
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 309 RAAVSSMCREAGLSEWS-QPIYVGNDEHKP--LREW----FVIVIMATIFILLISLI 361
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Qy 363 LRKPNTYKMP 374
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 362 CKICHLWIKLFP 373
      : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |

RESULT 12
US-08-442-282-14
; Sequence 14, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-282-14
```

```
;
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-281-14

Query Match          14.8%; Score 310.5; DB 1; Length 396;
Best Local Similarity 26.6%; Pred. No. 1.2e-23;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPQDFEIVDPCYGLYLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIIIT 86
DB 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIIT 82
QY 87 KNLHYKDGFDLKNKGIEAKIHLLPWQCTNGSEVSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAEHL-APPGSPGTSIVNLTCT 135
QY 147 -----YNNQYLL-CSWKEGIGVLLDTNINLFY---WYEGLDHALQCVDYIKAD 191
DB 136 TMTEDNYSRLRSQVSLHCTWLVGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSNKPPIRSSYFTFQLNIVKPLPPVYLFTFR 248
DB 190 LGRNIACWFPRTFTILSKGRDLWLVNGSSKHSARPPDQLFALHAIDQINPPLNVTAEI 249
QY 249 ESSCEIKLKWISPLGPPIPARCFDYEIEIREDDTTLVTATVENETTYTLKTTNETRQLCFVV 308
DB 250 EGT-RLSQWEKPVSAFPIHCFDYEIVKIHNTNRCYGLQIEKLTNAFTSIIDDLISKYDVQV 308
QY 309 RSKVNIYCSDDGIWSESDKOCWEGEDLSKTKTLRFLWLPFGFILL-----VIFVTGLL 362
DB 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLISLI 361
QY 363 LRKPNTPYKMP 374
DB 362 CKICHLWIKLFP 373

RESULT 13
US-08-442-281-14
; Sequence 14, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
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```
;
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-442-281-14

Query Match          14.8%; Score 310.5; DB 1; Length 396;
Best Local Similarity 26.6%; Pred. No. 1.2e-23;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPQDFEIVDPCYGLYLQWOPPLSLDHFKECTVEYELKYRNIGSETWKTIIIT 86
DB 25 DEKISLLPPVNFITKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIIT 82
QY 87 KNLHYKDGFDLKNKGIEAKIHLLPWQCTNGSEVSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAEHL-APPGSPGTSIVNLTCT 135
QY 147 -----YNNQYLL-CSWKEGIGVLLDTNINLFY---WYEGLDHALQCVDYIKAD 191
DB 136 TMTEDNYSRLRSQVSLHCTWLVGTDAPEDTQYFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSNKPPIRSSYFTFQLNIVKPLPPVYLFTFR 248
DB 190 LGRNIACWFPRTFTILSKGRDLWLVNGSSKHSARPPDQLFALHAIDQINPPLNVTAEI 249
QY 249 ESSCEIKLKWISPLGPPIPARCFDYEIEIREDDTTLVTATVENETTYTLKTTNETRQLCFVV 308
DB 250 EGT-RLSQWEKPVSAFPIHCFDYEIVKIHNTNRCYGLQIEKLTNAFTSIIDDLISKYDVQV 308
QY 309 RSKVNIYCSDDGIWSESDKOCWEGEDLSKTKTLRFLWLPFGFILL-----VIFVTGLL 362
DB 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLISLI 361
QY 363 LRKPNTPYKMP 374
DB 362 CKICHLWIKLFP 373

RESULT 14
US-08-939-727-14
; Sequence 14, Application US/08939727
; Patent No. 5916767
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,727
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
```

NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-939-727-14

Query Match 14.8%; Score 310.5; DB 2; Length 396;
Best Local Similarity 26.6%; Pred. No. 1.2e-23;
Matches 99; Conservative 70; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPDPDFEIVDPCGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWTKTIIT 86
Db 25 DEKISLLPPVNTTKVKG-LAQVLLQWKPNDQEQ-RNVNLEYQVKINAPKEDDIYTRIT 82
QY 87 KNLHYKDGFDLKNKIEAKIHTLLEPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
Db 83 ES---KCVTLHKFGSASVRILO--NDHSLASSWASAEHL-APGSPGTSIVNLCT 135
QY 147 -----YNNQYLL-CSWKGIGVLLDTNINLYF----WYEGDLHALQCVDYIKAD 191
Db 136 TTTTREDNYSLRYSQVSLHCTWLVTGTDAPEDTQFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFQLNIVKPLPPVLIATR 248
Db 190 LGRNIACFPFTFLSGRDLWLVNGSSKHSAIRPFDQALHAIDQINPPLNVTAEI 249
QY 249 ESSGEIKLWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETRQLCFV 308
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEIVKTHNRNGYLQIEKLMTNFAISIIDLSKYDVQV 308
QY 309 RSKVNYICSDGISEWSKOCWGEDLSKTKTLRFLWLPFGFIL-----VIFVTGLL 362
Db 309 RAAVSSMCREAGLSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI 361
QY 363 LRKPNTPYKMP 374
Db 362 CKICHLWIKLPP 373

RESULT 15
US-08-969-125-9
Sequence 9, Application US/08969125B
Patent No. 6143871
GENERAL INFORMATION:
APPLICANT: BONNEFOY, JEAN-YVES
GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,125B

FILING DATE: 12-No. 6143871-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 14.08; Score 295.5; DB 4; Length 427;
Best Local Similarity 26.08; Pred. No. 4.7e-22;
Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;

QY 11 LYTFLISTTFCGCTSSSDTEIKVNPDPDFEIVDPCGYLYLQWQPPLSLDHFKECTVEY- 69
Db 10 LWALLCAGGGGGGGAAPTETQPTVNLVSVENLCTVITWNPPEGAS--SNCSLWYF 67
QY 70 ---ELKYRNIGSETWTKTIITKNLHYKDGFDLKNKIEAKIHTLPLWQC-TNGSEVQSSWA 124
Db 68 SHFGDKQDKKIAPTERRSI-----EVLNERICLQVGS---QCSTNESEKPSILV 114
QY 125 ETTTWIS-PQGIPTKVQDMDCVYNNQYLLCSWKPGIGVLLDTNINLYFYEGDLHALQ 183
Db 115 EKC--ISPPEGDPESAVTELCQIWHNLSYMKCSWLPGRNTSPDNTYNTLYYHRSLEKTHQ 172
QY 184 CVDYIKADGQNGICRFPYLEASD--YKDFYICVNGSSSENKPIRSYFTFQLNIVKPLPP 241
Db 173 C-ENIFREGQYFGCSFDLTQVKSFEQHSQVQIMVKDNAGKIKPSFNIVPLTSRVKPPDP 231
QY 242 --VYLTTFTRESSCEIKLWSIPLGPIPARCFDYEIEIREDDT-----LYTATVENETY 293
Db 232 HIKNLSFHND--DLVQWENPQFI-SRCLFYEVENVNSQTETHNVFYVQEAECENPEF 287
QY 294 TLKTTNETRQLCFV-----RSKVNICY-SDDGIWSEWSKOCWGEDLSKK 339
Db 288 ERNVENTS---CFMVPGVLPDTLNTVIRVIRVTNKLVCYEDDKLWNSQEM-----SIGKK 339
QY 340 TLLRFWLPP-----GFILILVIFVTGL--LLRKPTVTP-KMIPFEFFCD 379
Db 340 RNSLYITMILLIVPVIAGAIIVLLLYLKRKLIIFPPIPDGPKIFKEMFGD 391

Search completed: September 1, 2001, 19:08:35
Job time: 162 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:54 ; Search time 15.95 Seconds
(without alignments)
1805.265 Million cell updates/sec

Title: US-09-077-817-12
Perfect score: 2087
Sequence: 1 MAFVCLAIGCLYTLFTTF.....TGILLRKPNTYPKMVRVTL 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	310.5	14.9	420	2 S21052	interleukin-5 rece
2	292	14.0	335	2 A40267	interleukin-5 rece
3	261	12.5	831	2 J01655	prolactin receptor
4	241	11.5	415	2 S12357	interleukin-5 rece
5	220	10.5	369	2 A42365	interleukin-2 rece
6	216.5	10.4	830	2 I50455	prolactin receptor
7	212.5	10.2	369	2 I49280	interleukin-2 rece
8	208	10.0	373	2 A55718	interleukin-2 rece
9	195	9.3	878	1 A40091	interleukin-3 rece
10	180.5	8.6	897	1 A39255	cytokine receptor
11	178	8.5	896	2 I56363	interleukin-3 rece
12	173.5	8.3	896	1 A35782	cytokine receptor
13	167	8.0	581	2 I45971	prolactin receptor
14	166	8.0	310	2 A29884	prolactin receptor
15	166	8.0	412	2 A41070	prolactin receptor
16	166	8.0	610	2 A36116	prolactin receptor
17	165	7.9	610	2 A34631	prolactin receptor
18	159	7.6	292	2 I77525	lactogen receptor
19	159	7.6	303	2 I77524	prolactin receptor
20	159	7.6	608	2 I53269	prolactin receptor
21	153	7.3	616	2 A30304	prolactin receptor
22	151	7.2	622	2 A40144	prolactin receptor
23	150.5	7.2	917	2 I49699	prolactin receptor
24	142.5	6.8	400	2 S06945	granulocyte-macrop
25	138	6.6	378	2 A40266	interleukin-3 rece
26	134.5	6.4	1097	2 S17308	leukemia inhibitor
27	133.5	6.4	333	2 S13684	granulocyte-macrop
28	133.5	6.4	378	2 S50040	granulocyte-macrop
29	131.5	6.3	630	2 I51086	prolactin receptor

ALIGNMENTS

RESULT 1

S21052
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S21052; S21053; A46175; S78106; S78107
R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 receptor.
A;Reference number: S21050; MUID:92121815
A;Accession: S21052
A;Molecule type: DNA
A;Residues: 1-420 <MUR>
A;Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A;Experimental source: clone lambda h5R.12
A;Accession: S21050
A;Molecule type: DNA
A;Residues: 1-395, 'I' <MU2>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A;Experimental source: clone lambda h5R.27
A;Accession: S21053
A;Molecule type: mRNA
A;Residues: 1-332, 'K' <MU3>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A;Experimental source: clone lambda h5R.25
R;Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A;Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum
A;Reference number: A46175; MUID:92357767
A;Accession: A46175
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 333-420 <TAV>
A;Experimental source: HL-60 cells and eosinophils
A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R;Murata, Y.
submitted to the EMBL Data Library, July 1991
A;Reference number: S78106
A;Accession: S78106
A;Molecule type: DNA
A;Residues: 1-128, 'I', 130-395, 'I' <MUW>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
R;Murata, Y.
submitted to the EMBL Data Library, September 1991
A;Reference number: S78107
A;Accession: S78107
A;Molecule type: mRNA
A;Residues: 1-128, 'I', 130-332, 'K' <MU4>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>

F:345-365/Domain: transmembrane #status predicted <TM>
F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 310.5; DB 2; Length 420;
Best Local Similarity 27.9%; Pred. No. 3.5e-17;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;

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QY 27 DTEIKVNPQDFEIVDPGGLYLYLQWQPPSLDHFRECTVEYELKYNIGSETWKIIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLLPPVFTIKVTG-LAQVLLQKPNPDQEQ-RNVNLVEYQVKNAPKEDDYET 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKDFGLNKGEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTLHKGFSAVRILQ---NDHSLASSWASAEHL-APGSPGTSVNLNLTCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYFY----WYEGLDHALQCVDIKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TTTTDDNYSLRYSQVSLHCTWLVGTDPEDTQYFLYRYGSWTE-----ECOEYSKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFQLNIVKPLPPVLTFR 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACWFPRTFILSKGRDLWLVNGSSKHSAIRPDFQALFALHAIQINPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLKWISPLGPAPCFDYEIEIREDDTTLVTATVENETYLTKTNETRLQCFVV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEYKIHNRNGYLOIEKLTNAFISIIDLSKYDVQV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 RSKYNIYCSDDGIWSEWSDKOCWGEDLSKTLIRFWLPFGFILLIVFVGLLL 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 RAAVSSMCREAGLWSEWS-QPIYGVNDEHKP--LREW----FVIVIMATICFILL 356
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 2
A:040267
Interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C:Accession: A40267
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tuytens, T.; Van der Heyden, J.; Fiers, W.; P
Cell 66, 1175-1184, 1991
A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-spec
A:Reference number: A40267; MUID:92005669
A:Accession: A40267
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <TAV>
A:Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
C:Keywords: cytokine receptor; transmembrane protein

Query Match 14.0%; Score 292; DB 2; Length 335;
Best Local Similarity 28.0%; Pred. No. 7.8e-16;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

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QY 27 DTEIKVNPQDFEIVDPGGLYLYLQWQPPSLDHFRECTVEYELKYNIGSETWKIIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLLPPVFTIKVTG-LAQVLLQKPNPDQEQ-RNVNLVEYQVKNAPKEDDYET 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKDFGLNKGEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTLHKGFSAVRILQ---NDHSLASSWASAEHL-APGSPGTSVNLNLTCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YNNQYLL-CSWKPGIGVLLDTNLYFY----WYEGLDHALQCVDIKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TTTTDDNYSLRYSQVSLHCTWLVGTDPEDTQYFLYRYGSWTE-----ECOEYSKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFQLNIVKPLPPVLTFR 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACWFPRTFILSKGRDLWLVNGSSKHSAIRPDFQALFALHAIQINPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLKWISPLGPAPCFDYEIEIREDDTTLVTATVENETYLTKTNETRLQCFVV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEYKIHNRNGYLOIEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKYNIYCSDDGIWSEWS 326
 :
Db 309 RAAVSSMCREAGLWSEWS 326
 :
RESULT 3
QY1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 186, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: JQ1655; MUID:93075121
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BA02439.1; PID:g222849
A:Experimental source: Kidney
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 12.5%; Score 261; DB 2; Length 831;
Best Local Similarity 26.3%; Pred. No. 7.3e-13;
Matches 98; Conservative 55; Mismatches 175; Indels 44; Gaps 16;

```
QY 18 TFGCTSSSTEIKVN--PPQDFE---IVDPG-----YLGXYLQWQPPLSL 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 97 TTFNITVATNEIGSSSDPQYVDVTSIVQGPSVNLTLTKRSANIMYLWAKWSPPLA 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 DHFKECTVEYELKYNIGSETWKIITIKNLHYKDFGLNKGEAKIHTLLPWQCTNGSEV 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 157 DASSNHLHYELRIKPEKEEWETI---SVGVQTCQKINR-LNAGMYVYVQVRCITDPGE 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 QSSWAETTYWISPOG-IPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYFYVEGL 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 WSESSSERHILIPGQSPPEKPTIIKRSPEKETFTCWKRPGLDGGHPTNTLLYSKEGE 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 DHALQCVDIKADGQNTGCRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQLNIVKP 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 EQVVECPDY-RTAGPN-SCYFDKKHTSFWTIYITVRATNEMSGNSDDPHYVDVYIVQP 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 239 LPPVYLFTRESCEIK-----LWS-IPLGPAPARCFDYEIEIR---EDDTTLVTAVEN 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 331 DPPVNVTLLELKPINRKPVLVLTWSPPLADVRSWGLTLEYELKPEGEWEWETIFVQG 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 ET-YTLKTTNETROLCFWRSKVNIVYCSDD--GIWSEWSKQWE-GEDLSKTLIRFWL 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 391 QTOYKMFSLNPKKYI-----IQHCKPDHGGSSSESNYIQIPNDFVKDMI-VWI 443
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 347 PFGFILLIVFV 358
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 444 VLGVLSLICLI 455
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 4
S12357
Interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S12357
R:Takaki, S.; Tomimaga, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu
EMBO J. 9, 4367-4374, 1990

A;Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A;Reference number: S12357; MUID:91092260

A;Accession: S12357

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-415 <TAK>

A;Cross-references: GB:090205; NID:g220465; PIDN:BAA14231.1; PID:g220466
C;Keywords: cytokine receptor; transmembrane protein

Query Match 11.5%; Score 241; DB 2; Length 415;
Best Local Similarity 24.9%; Pred. No. 1.2e-11;
Matches 88; Conservative 65; Mismatches 144; Indels 56; Gaps 17;
QY 34 PPQDFEIVDGYLYLQWOPPLSLDHFKECTVEYELKYNIGSETWTKTIITKNLHYKD 93
DB 29 PVVNFITKATG-LAQLVLLHWPNDQEQ-RHVLDLHYHVKINAPQDEYDTRKTES---KC 83
QY 94 GFDLNGKIEAKIHLLPWQCTNGSEVOSSNAETTYWISPOGIPETKVQDMDCVYVYN---- 149
DB 84 VTPLHEGFAASVRILK---SSHTTLASSWVSDEL-KAPPGSPGTSVTNLCTTHTTVVSS 139
QY 150 -----WQY-LLCSSKPCIGVLLDTNINLFWYEGDLHALQCVDIK-ADQONIGCRFP- 200
DB 140 HTHLRPYOVSLURCTWLVGKADAPDTQFLYRFGVLTE--KCQEYSRDLNNTACWPPR 197
QY 201 -YLEASDYKDFYICVNGSSENKPIRSSYFTFQLOINIVKPLPPVYLTFTRESSCEIKLKW 259
DB 198 TFINSKFEQLAVHINSSKRAAKLPDQLESPLAIDOVNPRNVTVEIESN-SLYIQWE 256
QY 260 IPLGPPIPARCFDYETIRED-----TTLVTATVENETTLKTNETRLQCLFVV 308
DB 257 KPLSAFPHDHCNVELKIYTNKNGHIQKEKLIANKFISKIDVDYSYIQ-----V 305
QY 309 RSKYNIYVSDGCIWSESDKOCWEGEDLSKTLRFV----LPGFILLIVIF 357
DB 306 RAAVSSPCRMPPGRGWS-QPIYVGKE--RKSLVE-WHLIVLPTAACFVLLIF 354

RESULT 5

A42565

Interleukin-2 receptor gamma chain - human

C;Species: Homo sapiens (man)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C;Accession: A42565; A46591; I54332

R;Takeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.;

Science 257, 379-382, 1992

A;Title: Cloning of the gamma chain of the human IL-2 receptor.

A;Reference number: A42565; MUID:92335883

A;Accession: A42565

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid; protein

A;Residues: 1-369 <TAK>

A;Cross-references: GB:D11086; NID:g303611; PIDN:BAA01857.1; PID:g219890

A;Experimental source: MOLT beta lymphoid cells

A;Note: sequence extracted from NCBI backbone (NCBIP:109167)

R;Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.

J. Biol. Chem. 268, 13601-13608, 1993

A;Title: Characterization of the human interleukin-2 receptor gamma chain gene.

A;Reference number: A46591; MUID:9233887

A;Accession: A46591

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-369 <RES>

A;Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058

R;Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; He

Hum. Mol. Genet. 2, 1099-1104, 1993

A;Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-link

A;Reference number: I54332; MUID:94004847

A;Accession: I54332

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-369 <RE2>

A;Cross-references: GB:L19546; NID:g349631; PIDN:AAC37524.1; PID:g349632
C;Genetics:

A;Gene: GDB:IL2RG; SCIDX1; IMD4

A;Cross-references: GDB:134807; OMIM:308380

A;Map position: Xq13.1-Xq13.1

A;Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3

A;Note: defects are associated with an X-linked form of severe combined immunodeficie
C;Superfamily: interleukin-2 receptor gamma chain

C;Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

Query Match 10.5%; Score 220; DB 2; Length 369;
Best Local Similarity 25.5%; Pred. No. 4.7e-10;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;
QY 97 LNKIGIEAKIHLLPWQCTNGSE-VQSSWAETTYWISPOGIPETKVQDMDCVYVWQYLLC 155
DB 19 LGVGLNTTILF-----PNGNEDTADFFLTMTDLSVSTLPLPEVQCFFVNFVYVNC 72
QY 156 SW-----KPGIGVLLDTNINLFWYEGDLH--ALQCVDIKADQONIGCRFPYLEASDY 207
DB 73 TWNSSEPPQ-----TNLTLYWYKNSDNDKVQKSHLYFSEITSGCQLQKKEIHL 125
QY 208 KDFYICVNGSSENKPIRSSYFTFQLOINIVKPLPPVYLTFTRESSCEIKLWISPLGPIPA 267
DB 126 QTFVVLQDPRE--PRQATQMLKQLNVLIPWAPENLTLLHLSQSLQELNNW---NRFLN 180
QY 268 RCFDYETEIRDD-TTLVTATVE-NEYTLKTNETRLQCFVRSKYNVYSDGGINSEW 325
DB 181 HCLEHLVQYRTDWDHSTEQSVDYRHKFSPLSPVQDQKRYTFVRSRFPLCGSAQHSW 240
QY 326 SDKQWEGEDLSKTLRLFWLPPFGFILILVIFVTG 360
DB 241 SHPIHW-GSNTSKEN-----PFLFALEAVVISVG 268

RESULT 6

I50455

prolactin receptor - pigeon

C;Species: Columba livia (domestic pigeon)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000

C;Accession: I50455

R;Chen, X.; Horseman, N.D.

Endocrinology 135, 269-276, 1994

A;Title: Cloning, expression, and mutational analysis of the pigeon prolactin recepto

A;Reference number: I50455; MUID:94293267

A;Accession: I50455

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-830 <CHE>

A;Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382

C;Superfamily: cytokine receptor homology

F;36-220/Domain: cytokine receptor homology <CRS1>

F;240-426/Domain: cytokine receptor homology <CRS2>

Query Match 10.4%; Score 216.5; DB 2; Length 830;
Best Local Similarity 24.4%; Pred. No. 2.5e-09;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;
QY 18 TTFGCTSSDTEIKVNPQDPFEIVDPGYLG-----YLYLQW 53
DB 97 TTYNTVWAMNEIGSNSS-----DPQYVDVTSIVQDPAPVNLSETKTSASTYLLAKW 150
QY 54 OPPLSLDHFKECTV-EYELKYNIGSETWTKTIITKNLHYKDFDLNKGIEAKIHTLLPMQ 112
DB 151 SPPLPADVTNSHVRYVELRLKPEKEWETV---SVGQYQYKYNR-LQAGVKYVQVR 206
QY 113 CTNGSEVQSSWAETTYWISPOG-IPEYKQVDMDCVYVWQYLLCSWKPGICGILLDTNVL 171
DB 207 CVLDIGSEWSEWSERHIHPNGESPEKPTIIKRSPKEFTTCWKPKSGGHPPTNTL 266
QY 172 FYWYEGDLHALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQ 231

Db 267 LYSKEGEBRVCEPDY-KTAGPN-SCYFDKKHTSFWIYNTVKTATNEIGSNVSDPLVVD 324
 QY 232 LQNIIVKPLPPVLTFTRESSCEIK-----LKWS-ITLGPPIPA--RCFYDEIETIREDDTTLY 284
 Db 325 VTYIVQTDPTTNNVLTLELKTNNRPYLVLTWSPPLADVRSGWLTLDYELRKPEEA--- 381
 QY 285 TATVENETITLKTNETRQLCFVY---RSKVNICYSDD--GIWSEWS-DKQCWEGEDLS 337
 Db 382 -----EWEETIFVQOQTHYKMFSLNPGKKYVQIHCKPDHGSSEWSLEKYLQIPTDFR 436
 QY 338 KKTLLRFWLPFGFLLILVIFV 358
 Db 437 IKDMV-VMIIVGVLSLILCV 456

RESULT 7
 I49280
 Interleukin-2 receptor gamma chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
 C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
 R:Caio, A.; Kozak, C.A.; Liu, Y.
 Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
 A>Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gene
 A:Reference number: A47514; MUID:93391374
 A:Accession: I49280
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <CAO>
 A:CROSS-references: EMBL:U21795; NID:G727349; PIDN:AAA64279.1; PID:G727350
 A:Accession: A47514
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-369 <RE2>
 A:CROSS-references: GB:L20048; NID:G404067; PIDN:AAA39286.1; PID:G404068
 R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
 Biochem. Biophys. Res. Commun. 193, 356-363, 1993
 A>Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of function
 A:Reference number: JN0592; MUID:93277575
 A:Accession: JN0592
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-369 <KUM>
 A:CROSS-references: DDBJ:D13565; NID:G303684; PIDN:BAA02760.1; PID:G303685
 R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
 Gene 130, 303-304, 1993
 A>Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
 A:Reference number: JN0775; MUID:93366191
 A:Accession: JN0775
 A:Molecule type: mRNA
 A:Residues: 1-369 <KOB>
 A:CROSS-references: GB:D13821; NID:G436045; PIDN:BAA02974.1; PID:G436046
 R:Chiu, R.K.; Dougherty, G.J.
 submitted to the EMBL Data Library, October 1993
 A>Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
 A:Reference number: S37582
 A:Accession: S37582
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
 R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
 Eur. J. Immunol. 24, 3014-3018, 1994
 A>Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal location
 A:Reference number: I53398; MUID:95104285
 A:Accession: I53398
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-369 <RES>
 A:CROSS-references: GB:S75852; NID:G861554; PIDN:AAB32904.1; PID:G861555
 C:Genetics:
 A:Gene: IL-2Rgamma

A: Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
 C: Complex: The high affinity receptor is a heterotrimer of alpha (see PIR-UHMS2), beta
 eptors.
 C:Function:
 A:Description: receptor for interleukin-2
 A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
 C:Superfamily: interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
 F:256-284/Domain: transmembrane #status predicted <TM>
 F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 10.2%; Score 212.5; DB 2; Length 369;
 Best Local Similarity 26.9%; Pred. No. 1.9e-09;
 Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

QY 136 PETKVQDMDCVYNNQYLLCSW----KPGIGVLLDTNNLFYWEYGLDHAL--OCVDYIK 189
 Db 53 PTLPLPEVQCFVFNIEYMNCTWNSSEPPQA-----TNLTLYRYKVSNDWTFQECSHYLF 107
 QY 190 ADGONICGRFPYLEADYKDFYICVNGSSSENKPIRSSYFTFQIQNIYKPLPPVYLTFRE 249
 Db 108 SKEITSGCQIKEDIQLYQTFVVL--ODPKPQRAVQKLNQLNVLIPRAPENLTLSNL 165
 QY 250 SSCEIKLKWSITPLGPIPARCFDEYIEIREDDITLVLTATVENE--TYTLKTTNETRQLCFV 307
 Db 166 SESOLELRWK--SRHIKERCLQYLVOYRSNRDRSWTELVNHEPRFSLPSVDELKRYTFR 223
 QY 308 VRSKVNICYSDDDGIWSEWSKQCEG----EDLSKTKLLRFWLPFGF--ILILVIFVTGL 361
 Db 224 VRSRYNPGSSQWQSKSQPVHWSHTVEENPSLFAELVLPVGTMLITLITLIFYVCW 283
 QY 362 LLRKPNTPY 370
 Db 284 LERMPPIPP 292

RESULT 8
 A55718
 Interleukin-2 receptor gamma chain precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
 C:Accession: A55718
 R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg
 Genomics 23, 69-74, 1994
 A>Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combi
 A:Reference number: A55718; MUID:95130114
 A:Accession: A55718
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-373 <HEN>
 A:CROSS-references: GB:U04361; NID:G517411; PIDN:AAC48403.1; PID:G517412
 C:Superfamily: interleukin-2 receptor gamma chain
 C:Keywords: cytokine receptor; duplication

Query Match 10.0%; Score 208; DB 2; Length 373;
 Best Local Similarity 26.0%; Pred. No. 4.3e-09;
 Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;

QY 115 NGSE-----VOSSWAEETTYWISPOGIPETKYQDMDCVYNNQYLLCSW-----KPGI 161
 Db 31 NGNEDITPDPFLFATPSET---LSVSSLPLPEVQ---CFVFNVEYMNCTWNSSEPPR-- 82
 QY 162 GVLLDTNLYNLYWYEGF--DHALQCVDYIKADGONICGRFPYLEADYKDFYICVNGSS 219
 Db 83 -----TNLTLYRYKVSNDKQVCEGHYLSREVTAACWQKEEIHLYETFVVLQRPRE 137
 QY 220 NKPIRSSYFTFQIQNIYKPLPPVYLTFRESSCEIKLWSITPLGPIPARCFDEYIEIREDD 279
 Db 138 --PRQSTQKLQNLVLPAPENLTUHLNLSQSLWS---NRHLDHCLHEHVQVVRSD 192

[illegible]

A;Accession: I56563
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-896 <RES>
A;Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
C;Genetics:
A;Gene: r1l-3beta
C;Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C;Keywords: cytokine receptor
F;39-235/Domain: cytokine receptor homology <CRS1>
F;253-433/Domain: cytokine receptor homology <CRS2>

Query Match 8.5%; Score 178; DB 2; Length 896;
Best Local Similarity 21.4%; Pred. No. 3.2e-06;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY 5 CLATGCL--YT-FLISTTGGTSSDTEIKVN-----PPQDFEIVDPGYLGY 49
DB 94 CVPRRCVLPYTFQSVSKEDYSLQPDRLSLHLVPLAQHVQPPPKDISPSG--DHF 151
QY 50 YLOWQPLP---SLDHFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLKNKGIEAKIH 106
DB 152 LKWSVPLGDAQVLLSOKDQFEVAYKQL-QDSWED--ASSLH-----TCNLWVTLPEPK 203
QY 107 TLPL-----WQCTNGSEVQ---SSWAETTYWISPGIPETKVKQDMDCVYNNWQVLL 154
DB 204 LFLPNSIVARVRAQLAPGSSLSGRPSGMSPEVHWDSETE-DKARPQNLCQFFDGIQSLN 262
QY 155 CSWAPGIGVLLDTNNLFYWEYGLDHALQCVDIYKADGQNTGCRFPYLEASDYKDFYICV 214
DB 263 CSWEVWTVTDVSFGLFYSSPKAGEKKSPVVK-----LQASRYTRYHCSL 311
QY 215 NGSENKPIRSSYTFQLOQ-----NIVKPLP-VYLTFTRESSCEIKLKWISPL 262
DB 312 NVSD---PAHSQYTVSVKRLQCKFTIESFNHIOQNPPTLNLTNRDS---YSLHWETQK 365
QY 263 GPIPARCFDYIEIR-----EDDTTLVTATVENETTYTLKTNETRQLCFVVRKSVNIYC 316
DB 366 MSYFPFIOHAFQVQYKKLDRWEDSKT---ENLNHNSMDLPQLEPGTSCYCARVRKTI 421
QY 317 SDDGIWSWSKQWEGDLSKTKLLRFPGLFILLIVFTVGLLL 363
DB 422 EYKGLWSEWSNECTWT-TDWVWPTL---WI-----VLILVFLILTLL 460

RESULT 12
A35782
cytokine receptor common beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A35782
R;Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A;Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protein
A;Reference number: A35782; MUID:90319131
A;Accession: A35782
A;Molecule type: mRNA
A;Residues: 1-896 <GOR>
A;Cross-references: GB:M34397; NID:g191821; PIDN:AAA37204.1; PID:g309101
C;Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptors
C;Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C;Keywords: cytokine receptor; duplication; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-896/Product: cytokine receptor common beta chain #status predicted <MAT>
F;23-441/Domain: extracellular #status predicted <EXT>
F;39-235/Domain: cytokine receptor homology <CRS1>
F;253-434/Domain: cytokine receptor homology <CRS2>
F;442-463/Domain: transmembrane #status predicted <TM>
F;464-896/Domain: intracellular #status predicted <INT>

Query Match 8.3%; Score 173.5; DB 1; Length 896;

Best Local Similarity 20.7%; Pred. No. 7.3e-06;
Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;

QY 5 CLATGCLYTFELISTTFFGCTSS-----SSDTEIK-----VNPQDFEIVDPGYLGY 48
DB 94 CVPRRCVPIPY---TRFSITNEDYYSFRPDSGLQIMVPLAQNVQPPPLKPNVSISSSEDR 150
QY 49 LYLOWQPLP---SLDHFKECTVEYELKYNIGSETWKTITKN-----LHYKDGFDLKNKG 100
DB 151 FLEWVSLSLGDQAQVSWLSKSDIEFEVAYKRL-QDSWEDAYSLSHTSKFQVNFEPKFLPNS 209
QY 101 IEA-KIHT-LLPWOCTNGSEVQSSWAETTYWISPGIPETKVKQDMDCVYNNWQVLLCSWK 158
DB 210 IYAPRVTRTRYPGSSLSGR--PSRWSPEAHWDSPG-DKAQPQNLCQFFDGIQSLHCSWE 266
QY 159 PGIGVLLDTNNLFYWEYGLDHALQCVDIYK-ADGQNI---GCRFPYLEASDYKDFYIC 213
DB 267 VWTQTTGSVSGFLFYRSPVAPEEKSPVVKPEPPGASVYTRYHCSLSPVPEPSAHSQYTVS 326
QY 214 VNGSENKPIRSSYTFQLOQIVKPLPPVYLTFTRESSCEIKLKWISPLGPIPARCFDYE 273
DB 327 V-----KHLEQCKFIMSYNHIQMEPTLNLTNRDS---YSLHWETQKWAYSIEHTFQ 377
QY 274 IEIREDDTLVTATVEN--EYTLKTNETRQLCFVVRKSVNIYCSDDGIWSWSKQCV 331
DB 378 VQYKKSDSWEDSKTENLDRHNSMDLSOLEPDTSCYCARVRKVPISNYDGIWSKWSEETV 437
QY 332 EGEDLSKTKTLRFPGLFILLIVFTVGLLL 363
DB 438 K-TDWVWPTL---WI-----VLILVFLILTLL 461

RESULT 13
I45971
prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C;Accession: I45971
R;Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
A;Reference number: I45971; MUID:93246019
A;Accession: I45971
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-581 <SCO>
A;Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C;Genetics:
A;Gene: PRLR
C;Superfamily: cytokine receptor homology
F;36-221/Domain: cytokine receptor homology <CRS>

Query Match 8.0%; Score 167; DB 2; Length 581;
Best Local Similarity 28.5%; Pred. No. 1.4e-05;
Matches 72; Conservative 36; Mismatches 121; Indels 24; Gaps 11;

QY 136 PETKVDMDCVYNNWQVLLCSWKPGIGVLLDTNNLFYWEYGLDHALQCVDIYKADGQNI 195
DB 27 PPEKPKLVKRSFGKETFTCWWEFGADGLPTNLTLYHKEGETLIHECPDY-KTGGPN- 84
QY 196 GCRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQLOQIVKPLPPVYLTFTRESSCEIK 255
DB 85 SCFESKHTSINKMYVTVMVAINQMGISSSDPLVHVHYIIVEPEPPANLLELKHPEDRK 144
QY 256 ----LKWSIP-LGPIPARCF--DYIEIREDDTLVTATVENET-YTLKTTN-ETROLCF 306
DB 145 PYLWIKWSPPTMDVKSGWFIQYIEIRLKPEKAT-----DWETHFTLKQTLKIFNLYP 198
QY 307 VVRKSVNIYCS-DDGIWSWSKQCV--GEDLSKTKTLRFPGLFILLIVFTVGLLL 363
DB 199 GQYLVQIRCKPDHGWSEWSPESSIQIPNDFPVKDTSMWIFVAILSAVICLIWVAVAL 258

A41070
prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 28-Jul-2000
C:Accession: A41070; I55417
R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin
A:Reference number: A41070; MUID:92041834
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALI>
A:Cross-references: GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390
R:O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
A:Reference number: I55417; MUID:95014432
A:Accession: I55417
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:17:44 ; Search time 13.12 Seconds
(without alignments)
986.934 Million cell updates/sec

Title: US-09-077-817-12

Perfect score: 2087

Sequence: 1 MAFVCLAIAGLYFLISTTF.....TGLLLRKNTYPMVRCVTL 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2059	98.7	380	1	IL32 HUMAN
2	309.5	14.8	420	1	IL5R HUMAN
3	294.5	14.1	424	1	IL31_MOUSE
4	294.5	14.1	427	1	IL31_HUMAN
5	261	12.5	831	1	PRLR_CHICK
6	241	11.5	415	1	IL5R_MOUSE
7	238	11.4	831	1	PRLR_MELGA
8	220	10.5	369	1	CYRG_HUMAN
9	216.5	10.4	830	1	PRLR_COLLI
10	212.5	10.2	369	1	CYRG_MOUSE
11	208	10.0	373	1	CYRG_CANFA
12	195	9.3	878	1	IL3B_MOUSE
13	189.5	9.1	379	1	CYRG_BOVIN
14	178.5	8.6	897	1	CYRB_HUMAN
15	173.5	8.3	896	1	CYRB_MOUSE
16	167	8.0	581	1	PRLR_BOVIN
17	166	8.0	610	1	PRLR_RAT
18	159	7.6	608	1	PRLR_MOUSE
19	153	7.3	616	1	PRLR_RABIT
20	151	7.2	862	1	PRLR_HUMAN
21	151	7.2	862	1	IL2S_HUMAN
22	150.5	7.2	917	1	IL6B_MOUSE
23	150	7.2	581	1	PRLR_CEREL
24	142.5	6.8	400	1	GMCR_HUMAN
25	138	6.6	378	1	IL3R_HUMAN
26	134.5	6.4	1097	1	LIFR_HUMAN
27	131.5	6.3	630	1	PRLR_ORENI
28	128	6.1	874	1	IL2S_MOUSE
29	126.5	6.1	918	1	IL6B_HUMAN
30	120.5	5.8	836	1	GCSR_HUMAN
31	113.5	5.4	1165	1	LEPR_HUMAN
32	112.5	5.4	1630	1	PTPL_DROME
33	109.5	5.2	918	1	IL6B_RAT

34 107.5 5.2 638 1 GHR_HUMAN
35 107.5 5.2 837 1 GCSR_MOUSE
36 107 5.1 634 1 GHR_BOVIN
37 106 5.1 634 1 GHR_SHEEP
38 105 5.0 511 1 VGLG_VSVO
39 104.5 5.0 1092 1 LIFR_MOUSE
40 102.5 4.9 638 1 GHR_PIG
41 101.5 4.9 638 1 GHR_RABIT
42 99.5 4.8 1162 1 LEPR_RAT
43 99 4.7 638 1 GHR_RAT
44 98.5 4.7 1162 1 LEPR_MOUSE
45 98 4.7 511 1 VGLG_VSVIG

PI0912 homo sapien
P40223 mus musculus
P79108 bos taurus
Q28575 ovis aries
P04884 vesicular s
P42703 mus musculus
P19756 sus scrofa
PI9941 oryctolagus
O62959 rattus norv
P16310 rattus norv
P48336 mus musculus
P04883 vesicular s

ALIGNMENTS

RESULT 1
IL32_HUMAN
ID IL32_HUMAN STANDARD; PRT; 380 AA.
AC Q14627; O00667;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13
DE BINDING PROTEIN).
GN IL13RA2 OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=96279273; PubMed=8663118;
RA Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N.,
RA Ferrara P.;
RT "Cloning and characterization of a specific interleukin (IL)-13
RT binding protein structurally related to the IL-5 receptor alpha
RT chain.";
RL J. Biol. Chem. 271:16921-16926(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H.,
RA Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97321053; PubMed=9177784;
RA Guo J., Apiou F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;
RT "Chromosome mapping and expression of the human interleukin-13
RL receptor.";
RL Genomics 42:141-145(1997).
CC -I- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13
CC (IL-13), BUT NOT TO IL-4.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X95302; CAA64617.1; -;
DR EMBL; U70981; AAB17170.1; -;
DR EMBL; Y08768; CAA70021.1; -;
DR MIM; 300130; -;

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DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3.1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT DISULFID 184 197
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B562C887 CRC64;

Query Match 98.7%; Score 2059; DB 1; Length 380;
Best Local Similarity 99.7%; Pred. No. 4.4e-161;
Matches 372; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPDPQFEIYDVGILYGLYQWOPPLSLD 60
Db 1 MAFVCLAIGCLYTLISTFTGCTSSDTEIKVNPDPQFEIYDVGILYGLYQWOPPLSLD 60
Qy 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHLLPQCNTNGSEVQ 120
Db 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHLLPQCNTNGSEVQ 120
Qy 121 SSWAETTWISQGPETKVDQDCVYVNWQYLLCSWKPGLVLDITNLYFYWEGLDH 180
Db 121 SSWAETTWISQGPETKVDQDCVYVNWQYLLCSWKPGLVLDITNLYFYWEGLDH 180
Qy 181 ALQCVDYIKADQNTGCRFPYLEASDYKDFICVNGSENKPIRSSYFTFQIQNIVKPLP 240
Db 181 ALQCVDYIKADQNTGCRFPYLEASDYKDFICVNGSENKPIRSSYFTFQIQNIVKPLP 240
Qy 241 PVLFTFTRESSECEIKLWSIPLGPAPCFDYEIREDDTTLVATVENEYTLTKTNE 300
Db 241 PVLFTFTRESSECEIKLWSIPLGPAPCFDYEIREDDTTLVATVENEYTLTKTNE 300
Qy 301 TRLQCFVVRVSVNYCSDGIGWSEMSDKQCEGEDLSKTLRLFWLPGFTILIVIFVTG 360
Db 301 TRLQCFVVRVSVNYCSDGIGWSEMSDKQCEGEDLSKTLRLFWLPGFTILIVIFVTG 360
Qy 361 LLLRKPNTYPRMW 373
Db 361 LLLRKPNTYPRMI 373

RESULT 2
IL5R_HUMAN
ID IL5R_HUMAN STANDARD; PRT; 420 AA.
AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125
DE ANTIGEN).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBITaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
[2]

SEQUENCE FROM N.A.
RP MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;
RT "Molecular basis of the membrane-anchored and two soluble isoforms of
RT the human interleukin 5 receptor alpha subunit.";
RL Interleukin-5 Receptor Alpha-2 Chain.
RN Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
[3]
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=92005669; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of
RT an IL5-specific alpha chain and a beta chain shared with the receptor
RT for GM-CSF";
RL Cell 66:1175-1184(1991).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".
-----
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EMBL; M96652; AAA59152.1; -
EMBL; M96651; AAA59151.1; -
EMBL; M75914; AAA36110.1; -
EMBL; A26249; CAA01793.1; -
EMBL; A24587; CAA01731.1; -
EMBL; A26251; CAA01794.1; -
EMBL; A40267; A40267.
PIR; A40267; A40267.
MIM; 147851; -.
InterPro; IPR000950; -.
InterPro; IPR002465; -.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420
FT DOMAIN 21 342
FT TRANSMEM 343 362
FT DOMAIN 363 420
FT CARBOHYD 35 35
FT CARBOHYD 131 131
FT CARBOHYD 216 216
FT CARBOHYD 244 244
FT VARSPLIC 333 335
FT VARSPLIC 336 420
FT VARSPLIC 333 333
FT VARSPLIC 334 420
SQ SEQUENCE 420 AA; 47700 MW; 420681FBC6B51700 CRC64;
INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
NDE -> FSR (IN SOLUBLE ISOFORM S1).
MISSING (IN SOLUBLE ISOFORM S1).
N -> K (IN SOLUBLE ISOFORM S2).
MISSING (IN SOLUBLE ISOFORM S2).
Query Match 14.8%; Score 309.5; DB 1; Length 420;
Best Local Similarity 27.6%; Pred. No. 4.4e-19;
Matches 98; Conservative 65; Mismatches 151; Indels 41; Gaps 15;

Qy 27 DTEIKVNPDPQFEIYDVGILYGLYQWOPPLSLDHFECTVEYELKYRNIGSETWKTIT 86
Db 25 DEKISLLPPVNTIKVTG-LAQVLLQWKPDPQEQ-RNVNLEYQVKINAPDEDDYETRIT 82
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DR	EMBL; S80963; AAB50695.1; -
DR	MG; MG1:105052; I113ra.
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW	RECEPTOR; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT	SIGNAL 1 25 POTENTIAL.
FT	CHAIN 26 424 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
FT	DOMAIN 26 340 EXTRACELLULAR (POTENTIAL).

RP SEQUENCE FROM N.A.
RC
RC TISSUE-Carcinoma;
RX MEDLINE=97165986; PubMed=9013879;
RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,
RA Ferrara P.;
RT "Cloning of the human IL-13R alpha chain and reconstitution with the
RT IL4R alpha of a functional IL-4/IL-13 receptor complex.";
RL FEBS Lett. 401:163-166(1997).
RN [2]
RN
RP SEQUENCE FROM N.A.


```
DR HSP; P16471; IBP3.
DR InterPro: IPR000950; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002465; -.
DR Pfam: PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT CARBOHYD 75 86
FT CARBOHYD 59 91
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94102 MW; 1C4E7579IDCABE9 CRC64;

Query Match 12.5%; Score 261; DB 1; Length 831;
Best Local Similarity 26.3%; Pred. No. 9, 4e-14;
Matches 98; Conservative 55; Mismatches 175; Indels 44; Gaps 16;

QY 18 TTFCTSSSTEIKVN--PQDFE---IVDPG-----YLGLYLQWQPPLSL 59
DB 97 TTFNITVATNEIGSSSDPQYVDVTSIVOPGSPVNLTLTKRSANIMYLAKWSPLLA 156
QY 60 DHFKECTVEVELKRNIGSETWTKIITKNLHYKDGFDLNGIEAKIHTLLPWQCTNGSEV 119
DB 157 DASSNHLHYELRLKPEKEWEI---SVGVQVQCKINR--LNAGMYVVOVRCITLDPGE 212
QY 120 QSSWAETTYWISPOG-IPETKVQDMDCVYVYVQYLLGCSWRKPGIGVLLDTNINFLFYWEGL 178
DB 213 WSESSERHILPSGQSPPEKPTIICKRSPKEFTTCKWPKGLDGHPTNTLYLSKEGE 272
QY 179 DHALQCVDIKADQNTGCRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQLQNIKVP 238
DB 273 EQVYECPDY-RTAGPN-SCYFDKKHTSFWTIYNTVTRATNMGSSNSDPPHYVDVYIVQP 330
QY 239 LPPVLTFTRESSCEIK---LKWS-IPLGPAPARCFDYEIR---EDDTLLVTATVEN 290
DB 331 DFPVNVILELKKPINRKPVLVLTWSPPLADVRSGWLTLEYELRLKPEEGEWETIFVGQ 390
QY 291 ET-YTLKTTNETROLCFVWRKSVKNYSDD--GIWSEWSDKQCWE--GEDLSKTKLLRFLW 346
DB 391 QTYQKMFSLNPGKKYI-----IQHCKPDHGGSWSESSSENYIQIPNDRVKDMI-VWI 443
QY 347 PFGILLIIVFV 358
DB 444 VLGVLSSLICLI 455

RESULT 6
ID IL5R_MOUSE STANDARD; PRT; 415 AA.
AC P21183;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA).
GN IL5RA OR IL5R.
OS Mus musculus (Mouse).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092260; PubMed=2265612;
RA Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RA Takatsu K.;
RT "Molecular cloning and expression of the murine interleukin-5
RL receptor.";
RL EMBO J. 9:4367-4374(1990).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
CC ON B-CELLS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
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CC -----
DR EMBL; D90205; BAA14231.1; -.
DR PIR; S12357; S12357.
DR MGD; MGI:96558; IL5ra.
DR InterPro; IPR000950; -.
DR InterPro; IPR002465; -.
DR PROSITE; PS01352; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 415
FT DOMAIN 18 339
FT TRANSMEM 340 361
FT DOMAIN 362 415
FT DISULFID 131 152
FT DISULFID 179 193
FT CARBOHYD 32 32
FT CARBOHYD 128 128
FT CARBOHYD 213 213
FT CARBOHYD 241 241
SQ SEQUENCE 415 AA; 46989 MW; A4326D2922571C08 CRC64;

Query Match 11.5%; Score 241; DB 1; Length 415;
Best Local Similarity 24.9%; Pred. No. 1, 7e-12;
Matches 80; Conservative 65; Mismatches 144; Indels 56; Gaps 17;

QY 34 PPQDFEIVDPGYLGLYLQWQPPLSLDHFKRECTVEYELKYNIGSETWTKIITKNLHYKD 93
DB 29 PPVNFITKATG-LAQVLLHNDPNPDQEQ-RHVDLEYHVKNAPQEDVDTRKTES---KC 83
QY 94 GFDLNGIEAKIHTLLPWQCTNGSEVSSNAETTYWISPOGIPETKVQDMDCVYVYV--- 149
DB 84 VTPLHEGFAASVRLTK---SSHTTLASSWVSABL-KAPPGSPGTSVTLNLTCTHTTVVSS 139
QY 150 -----WQY-LLCSWKPGIGVLLDTNINFLFYWESGLDHALQCVDIK-ADGQNIIGCRFP- 200
DB 140 HTHLRPYQVSLRCTLVWGKAPEDTQYLYRFGVLTE--KCQETSRDALNRNACFWPR 197
QY 201 -YLEASDYKDFYICVNGSSSENKPIRSYFTFQLQNIKVPPLPVLTFTRESSCEIKLWS 259
DB 198 TFINSKGEQLAVHINGSRRRAKKPDLQFSLAIDQVNPRTVETIESN-SLYIOWE 256
QY 260 IPLGPIPARCFDYEIREDD-----TTLVTATVENETTYLTKTTNETROLQCFVW 308
DB 257 KPLSAFPDHCNFYELKIYNTKNNGHIQREKLIANKFIKIDDVSTYSIQ-----V 305
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[illegible]

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```

CC EMBL; D11086; BAA01857.1; -.
CC EMBL; L12183; AAA59145.1; -.
CC EMBL; L12178; AAA59145.1; JOINED.
CC EMBL; L12176; AAA59145.1; JOINED.
CC EMBL; L12177; AAA59145.1; JOINED.
CC EMBL; L12179; AAA59145.1; JOINED.
CC EMBL; L12180; AAA59145.1; JOINED.
CC EMBL; L12181; AAA59145.1; JOINED.
CC EMBL; L12182; AAA59145.1; JOINED.
CC EMBL; L19546; AAC37524.1; -.
CC PIR; A42565; A42565.
CC PDB; 1ILM; 26-JAN-95.
CC PDB; 1ILN; 26-JAN-95.
CC MIM; 308380; -.
CC MIM; 300400; -.
CC InterPro; IPR000950; -.
CC InterPro; IPR001777; -.
CC InterPro; IPR002465; -.

Query Match      10.5%; Score 220; DB 1; Length 369;
Best Local Similarity 25.5%; Pred. No. 7.8e-11;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

Qy 97 LNKIEAKIHLLPWOCTNGSE-VQSSWAETTYWISQIGPETKVQDMDCVYVWQYLLC 155
Dy 19 LGVGLNTLITL-----PNGNEDTADFFLTMTPTDSLSVSTPLPEVQCFVNFVYVNC 72

Qy 156 SW-----KPGIGVLLDNYNLFVYEGLDH--ALQCVDIKADQNGICRFPYLEASDY 207
Dy 73 TWNSSESEPQ-----TNLTHWYKNSDNDKVKCCHYLFSSEITSGCOLQKKEIHLY 125

Qy 208 KDFYICVNGSSSENKPIRSSYFTFQIQNIVKPLPPVYLFTTRESSCEIKLKWISPLGPPEA 267
Dy 126 QTFVQLQDPRE--PRQATQMLQNLVLPWAPENLTLHLKLSQLELNNW---NRFNL 180

Qy 268 RCFDYETEIRSD-DTTLVTATVE-NETYLKTTNETQLCFVRSKVNICYSDDGISEW 325
Dy 181 HCLEHLVQYRTDWDHSTEQSVYRHKFLSPSDGQKRYTFRVRSRPNLPGSAQHSEW 240

Qy 326 SDKQCEGEDSKKTLRFLWLPFGFILILVFTVG 360
Dy 241 SHPIHW-GSNTSKEN-----PFLFAEAVVISVG 268

RESULT 9
PRLR_COLLI STANDARD; PRT; 830 AA.
AC Q90374; PRLR_COLLI STANDARD; PRT; 830 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cropsac;
RX MEDLINE=94283267; PubMed=7516866;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor."
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

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CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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EMBL; U07694; AAA20646.1; -.  

HSSP; P16471; IBP3.  

InterPro; IPR000950; -.  

InterPro; IPR001777; -.  

InterPro; IPR002465; -.  

Pfam; PF00041; fn3; 4.  

PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.  

Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  

SIGNAL 1 23  

CHAIN 24 830  

DOMAIN 24 439  

TRANSMEM 440 460  

CYTOPLASMIC (POTENTIAL).  

DOMAIN 25 122  

DOMAIN 123 226  

DOMAIN 229 326  

DOMAIN 327 429  

DISULFID 36 46  

DISULFID 75 86  

CARBOHYD 59 59  

CARBOHYD 91 91  

CARBOHYD 100 100  

CARBOHYD 112 112  

CARBOHYD 132 132  

CARBOHYD 263 263  

CARBOHYD 304 304  

CARBOHYD 316 316  

CARBOHYD 336 336  

SEQUENCE 830 AA; 94507 MW; 3B074E83CDF69EFF CRC64;



Query Match 10.4%; Score 216.5; DB 1; Length 830;  

Best Local Similarity 24.4%; Pred. No. 4e-10;  

Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;



Qy 18 TTFCTSSSTDEIKVNPQDFEIVDPGLG-----DPQYVDVTISVQPDAPVNLSTETKSASTTYLLAKW 150  

Dy 97 TTYNTVYVAMNEIGSNSS-----DPQYVDVTISVQPDAPVNLSTETKSASTTYLLAKW 150



Qy 54 QPPLSLDHFKECTV-EYELKYRNISETWKTITKLNHYKDGFLNKGIEAKIHLLPWO 112  

Dy 151 SPPLADVTNSHYRYELRLKPEKEWEIV---SVGVQYQVKNR-LQAGVYVQVR 206



Qy 113 CTNGSEVQSSWAETTYWISQIG-IPETKVQDMDCVYVWQYLLCSWPKGVGLDYNL 171  

Dy 207 CVLDIGSEWSSSRHIHPNGESPEKPTIIKCRSEKETFTCWKPKGSGDGHPTNYTL 266



Qy 172 FYWEGLDHALQVDYIKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQ 231  

Dy 267 LYSKEGEERYVECPDY-KTAGPN-SCYFDKKTHTSFWTYINITYKATNEIGSNVDPLVD 324



Qy 232 LQNIKPLPPVYLFTTRESSCEIK-----LKWS-IPLGPIPA--RCFDYETEIRSDDTTLV 284  

Dy 325 VTYIVQDPPVNVYTLKTKVNRKPYLVLTWSPPPLADVRSGWLTLDYELRKEPEA--- 381



Qy 285 TATVENETYTLKTTNETRQLCFVY-----RSKNVICYSDD--GIWSEWS-DKQCEGEDLS 337  

Dy 382 -----EEWETIFVQOQTHYKMFSLNPKGKYIVQIHCKPDHHSWSEWSLEKYLQIPTDFR 436



Qy 338 KKTLLRFLWLPFGFILILVIFV 358  

Dy 437 IKDMV-VMIIVGVLSLICLV 456


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RESULT 10
CYRG_MOUSE
ID CYRG_MOUSE STANDARD; PRT; 369 AA.
AC P34902;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277575; PubMed=8503926;
RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT "Cloning of the mouse interleukin 2 receptor gamma chain:
RT demonstration of functional differences between the mouse and human
RT receptors."
RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CBA/CA;
RA Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
RT Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93366191; PubMed=8359699;
RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RT gamma."
RL Gene 130:303-304(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104285; PubMed=7805729;
RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
RA Fischer A., de Saint Basile G.;
RT "The murine interleukin-2 receptor gamma chain gene: organization,
RT chromosomal localization and expression in the adult thymus."
RL Eur. J. Immunol. 24:3014-3018(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=B6.S;
RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
RA Dougherty G.J.;
RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT the adhesion protein CD44."
RL J. Neuroconcl. 26:231-239(1995).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC
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CC -----

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DR EMBL; D13821; BAA02974.1; -
 DR EMBL; U21795; AAA64279.1; -
 DR EMBL; D13565; BAA02760.1; -
 DR EMBL; L20048; AAA32986.1; -
 DR EMBL; S75852; AAB32904.1; -
 DR EMBL; S75844; AAB32904.1; JOINED.
 DR EMBL; S75845; AAB32904.1; JOINED.
 DR EMBL; S75847; AAB32904.1; JOINED.
 DR EMBL; S75848; AAB32904.1; JOINED.
 DR EMBL; S75849; AAB32904.1; JOINED.
 DR EMBL; S75850; AAB32904.1; JOINED.
 DR EMBL; S75851; AAB32904.1; JOINED.
 DR EMBL; X75337; CAA53085.1; -
 DR PIR; JN0775; JN0775.
 DR HSSP; P31785; ILIN.
 DR MGI; 96551; IL2rg.
 DR InterPro; IPR000950; -
 DR InterPro; IPR001777; -
 DR InterPro; IPR002465; -
 DR Pfam; PF00041; fn3; 1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 369 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
 FT DOMAIN 23 263 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 264 284 POTENTIAL.
 FT DOMAIN 285 369 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 151 250 FIBRONECTIN TYPE-III.
 FT DISULFID 62 72 POTENTIAL.
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 369 AA; 42241 MW; CB2D5AB459077AC7 CRC64;

Query Match 10.2%; Score 212.5; DB 1; Length 369;
 Best Local Similarity 26.9%; Pred. No. 3.2e-10;
 Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

QY 136 PETKVDMDCVYVNYOYLCSW----KPGIGVLLDTNVLNLFYVYEGLDHAL--OCVDYIK 189
 Db 53 PTLPLPVEQVCFVNFIEYMNCTWNSSEPQA-----TNLTLYRKVSDNNTFQBCSHYLF 107
 QY 190 ADGQNICRFPYLEADYKDFYICVNGSSSENKPIRSYFTFQIQNIYKPLPPVYLTFTRE 249
 Db 108 SKETSGCQIQKEDIQLYQYFVVQL--QDPKQPORRAVQKLNQNLVIRAPENLTLSNL 165
 QY 250 SSEIKLKWSIPGIPARCFDEIETRED-DITLVATVENE--TYTLKTTNETRQLCFV 307
 Db 166 SESOLELRWK--SRHIKERCLQVLYQVRSNRDRSWTEILVNHPEPRLSPSYDELKRYTFR 223
 QY 308 VRKVNIVCSDDGIWSEMSDKQWEG---EDLSKTKLLRFLWLPFGF--ILILVIFVTGL 361
 Db 224 VRKYNPISCCSQWSKWSQPVHMGSHVTVEENPSLFAELVLPVGMGLTIITIFVYCW 283
 QY 362 LLRRKPNTYP 370
 Db 284 LERMPPIPP 292

RESULT 11
 CYRG_CANFA
 ID CYRG_CANFA STANDARD; PRT; 373 AA.
 AC P40321;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)

DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).

GN IL2RG.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=95130114; PubMed=7829104;

RA Henthorn P.S., Somberg R.L., Finlani V.M., Puck J.M., Patterson D.F.,

RA Felsburg P.J.;

RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked

RT severe combined immunodeficiency is a homologue of the human

RT disease".

RL Genomics 23:69-74(1994).

CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF

CC INTERLEUKINS.

CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND

CC PROBABLY ALSO THE IL-13 RECEPTORS.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED

CC SEVERE COMBINED IMMUNODEFICIENCY.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

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CC -----

DR EMBL; U04361; AAC48403.1; -.

DR HSSP; P31785; IILN.

DR InterPro; IPR000950; -.

DR InterPro; IPR001777; -.

DR InterPro; IPR002465; -.

DR Pfam; PF00041; fn3.1.

DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 22

FT CHAIN 23 373

FT DOMAIN 23 261

FT TRANSFEM 262 283

FT DOMAIN 284 373

FT DOMAIN 151 249

FT DISULFID 62 72

FT DISULFID 102 115

FT CARBOHYD 24 24

FT CARBOHYD 71 71

FT CARBOHYD 75 75

FT CARBOHYD 84 84

FT CARBOHYD 159 159

FT CARBOHYD 164 164

FT CARBOHYD 249 249

SQ SEQUENCE 373 AA; 42516 MW; 03A0DE1F8B089DBB CRC64;

Query Match 10.0%; Score 208; DB 1; Length 373;

Best Local Similarity 26.0%; Pred. No. 7.5e-10;

Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;

Oy 115 NGSE-----VQSWAETTWISQGIPEKVKQDMDCVYNWQYLCSW-----APGI 161

Db 31 NGNEDITPDPFLTATPSET---LSVSSLPLPEVO---CFVFNVEYMNCTWNSSEPRP-- 82

Oy 162 GVLLDTNLYFYWYEGEL--DHALQCVDIKADGONIGRCFPELEASDYKDFYICVNGSSE 219

Db 83 -----TNLTLYHWYKNSNDKQVCEGHLYSREVTAGCWLOKEIHLXLYFVQLRDPRE 137

Oy 220 NKPIRSSYFTFQLQNTVVKPLPPVYLATFTRSSCEIKLWSIPLGPIPARCFDYEIREED 279

Db 138 --PRQSTQKQLQNLVWPAPENLTLNLSSEOLELSWS---NRHLDCLEHVQVRS 192

Oy 280 -DTLTVATVEN-ETYLTKTNETRQLCFVVRKSNVNYCSDGIGWSEWSKQWGEDLS 337

Db 193 WDRSWTEQSDVHRNFSPLSDGKFYFRVRSYRNPCLGSAORWSEWSHPHWHV-GSNTS 251

Oy 338 KKTLL----RFLPFGFILLVIVFV 358

Db 252 KENPLFASEAVLPLGSMGLIISLI 276

RESULT 12

IL3B_MOUSE

ID IL3B_MOUSE STANDARD; PRT; 878 AA.

AC P26934;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE INTERLEUKIN-3 RECEPTOR CLASS II BETA CHAIN PRECURSOR (COLONY

DE STIMULATING FACTOR 2 RECEPTOR, BETA 2 CHAIN).

GN CSF2RB2 OR AIZCA OR IL3RB2 OR IL3R.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90117145; PubMed=2404337;

RA Itoh N., Yonehara S., Schreurs J.J., Gorman D.M., Maruyama K., Ishii A.,

RA Yahara I., Arai K., Miyajima A.;

RT "Cloning of an interleukin-3 receptor gene: a member of a distinct

RT receptor gene family".

RL Science 247:324-327(1990).

CC -1- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3

CC RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE

CC OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5

CC AND GM-CSF RECEPTORS.

CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -----

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CC -----

DR EMBL; M29855; AAA39295.1; -.

DR PIR; A40091; A40091.

DR MGD; MGI:1339760; Csf2rb2.

DR InterPro; IPR000950; -.

DR InterPro; IPR001777; -.

DR InterPro; IPR002465; -.

DR Pfam; PF00041; fn3.2.

DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 22

FT CHAIN 23 878

FT DOMAIN 23 440

FT TRANSFEM 441 462

FT DOMAIN 463 878

FT DISULFID 39 49

FT DISULFID 78 95

FT DISULFID 254 264

FT DISULFID 293 310

FT CARBOHYD 62 62

FT CARBOHYD 350 350

SQ SEQUENCE 878 AA; 97195 MW; 8EBC909ZADC24D56 CRC64;

Query Match 9.3%, Score 195; DB 1; Length 878;
 Best Local Similarity 24.1%; Pred. No. 2.5e-08;
 Matches 86; Conservative 59; Mismatches 150; Indels 62; Gaps 23;

QY 34 PPQDFEIVDPGLYGLVLOWQPLP---SLDFKCECTVEYELKYNIGSETWKTITNLH 90
 Db 139 PKDHIHSPSG---DHFLELSSVSGDSQVSWLSDKIDFEVAYKRL-ODSWED--ASSLH 193
 QY 91 YKDFDNLKNGIEAKIHTLLP-----WQCTNGSEVQ-----SSWAETTYWISPGQIPET 138
 Db 194 -TSNFQVN--LEPKL--FLPNSIYAARVRLSAGSSLSGRPSRWSPEVHDSQF-DKA 247
 QY 139 KVQDMCVYVNWQYLLSGPGIGVLDNTNLYFYWEGLDHALQCVDYIKADQONI--- 195
 Db 248 QPQNLQCFDFDQISLHCSWEVMTQTTGSVSGFLFYRSPAAPEEKSPVVKPQASVTR 307
 QY 196 -GCRFPYLEADYKDFYICVNGSENPIRSSYFTFQNLQVTKPLPPVY-LTFRESCE 253
 Db 308 YRCSLPVPEPSAHSQYTVSVKHLQGGKFI-MSYVHIQME-----PILNQTKNRDS--- 357
 QY 254 IKLKWSTPLGPIPARCFD--YEIEIREDDTLVTATVEN-----ETYTLKTTNETRQLCFV 307
 Db 358 YSLHWETQKIP---KYDHTFQVQYKKKSEWKSDEKSTENLGRVNSMDLPQLEPDTSYCAR 414
 QY 308 VRSK-VNIYCSDDGIGWSESDKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTGLLL 363
 Db 415 VVRKPISDY---DGIWSEWSNEYTWT-TDWVMPYL---WI---VLILVFLIFLTL 460

RESULT 13
 CYRG_BOVIN STANDARD; PRT; 379 AA.
 AC Q95118;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
 DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
 GN IL2RG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96268473; PubMed=8672241;
 RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
 RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
 gamma gene";
 RL DNA Cell Biol. 15:453-459 (1996).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC -----
 CC EMBL: U33748; AAB07812.1; -
 CC HSP: P31785; IILN.
 CC InterPro: IPR000950; -
 CC InterPro: IPR001777; -
 CC InterPro: IPR002465; -

Pfam: PF00041; fn3; 1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
 FT DOMAIN 23 269 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 270 290 POTENTIAL.
 FT DOMAIN 291 379 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 158 256 FIBRONECTIN TYPE-III.
 FT DISULFID 68 78 POTENTIAL.
 FT DISULFID 109 122 POTENTIAL.
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 9.1%; Score 189.5; DB 1; Length 379;
 Best Local Similarity 26.2%; Pred. No. 2.5e-08;
 Matches 62; Conservative 42; Mismatches 106; Indels 27; Gaps 9;

QY 135 IPEKVDMDCVYVNWQYLLCSW-----KPGIGVLDNTNLYFYWY---EGLDHALQCV 185
 Db 61 LPLPKVQ---CFVENVEYMNCTWNSSEPQP-----NNLTHGYRNFNNGDKLQECG 110
 QY 186 DYKADQNTGICREPYLEASDYKDFYICVNGSENKPIRSSYFTFQNLQVTKPLPPVLT 245
 Db 111 HLFSEGITGCGWFGKKEIRLYETFFVQLODPREHR--KQPKQMLQDLVIPWAPENLT 168
 QY 246 FTRESCEIKLWSTPLGPIPARCFDYEIEIREDDTLVTATVEN-ETYTLKTTNETRQ 303
 Db 169 LRNLSEFQLELWS---NRYLDHCLHLVQYRSRDRSWSFQSVDRHSFSLPSVDAQKL 225
 QY 304 LCFVVRSKVNIYCSDDGIGWSESDKQCEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
 Db 226 YTFVRSRYPNLCGSAQHSWSDSYPIHW-GSNTSKENIENPENPSLFALEAVLIPLG 281

RESULT 14
 CYRG_HUMAN STANDARD; PRT; 897 AA.
 AC P32927;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR (CDW131 ANTIGEN).
 GN CSF2RB OR IL5RB OR IL3RB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91088571; PubMed=1702217;
 RA Havashida K., Kitamura T., Gorman D.M., Arai K., Yokota T.,
 RA Miyajima A.;
 RT "Molecular cloning of a second subunit of the receptor for human
 RT granulocyte-macrophage colony-stimulating factor (GM-CSF):
 RT reconstitution of a high-affinity GM-CSF receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9655-9659 (1990).
 RN [2]
 RP REVISION TO 454.
 RA Kitamura T.;
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
 CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:17:29 ; Search time 24.61 seconds
(without alignments)
2032.154 Million cell updates/sec

Title: US-09-077-817-12

Perfect score: 2087

Sequence: 1 MAFVCLAIGCLYELISTTF.....TGLLLRKNTPYKMWRCVTLL 378

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_prodent:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194.5	57.2	383	11	O88786 mus musculus
2	310.5	14.9	420	4	Q14633 homo sapien
3	309.5	14.8	396	4	Q14631 homo sapien
4	292	14.0	333	4	Q15469 homo sapien
5	291.5	14.0	415	11	Q920K4
6	264.5	12.7	349	6	Q97597 bos taurus
7	241.5	11.6	279	4	Q9UDY5
8	197.5	9.5	363	13	Q9DEQ1 oncorhynch
9	185.5	8.9	611	13	Q9PTI0 xenopus lae
10	185.5	8.9	611	13	Q9IBF6 xenopus lae
11	178	8.5	896	11	Q64146 rattus norv
12	173.5	8.3	881	13	Q57519 xenopus lae
13	172	8.2	611	13	Q9PTH9 xenopus lae
14	170	8.1	890	11	Q921A0 cavia porce
15	169	8.1	227	6	Q9GLW3 ursus marit
16	167	8.0	296	6	Q18880 bos taurus
17	167	8.0	622	6	Q9N0J7 callithrix
18	161	7.7	581	6	O46561 ovis aries
19	156	7.5	625	6	Q9XS92 trichosurus

ALIGNMENTS

RESULT 1	20	153.5	7.4	918	13	Q9W6U9
O88786	21	153	7.3	217	6	O46386
ID O88786	22	151	7.2	206	4	Q16354
AC O88786	23	151	7.2	349	4	Q9UJH5
DT 01-NOV-1998 (TREMBLrel. 08, Created)	24	147.5	7.1	538	13	Q9DFU0
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)	25	146.5	7.0	422	4	Q9UHH5
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	26	145.5	7.0	422	4	O75462
DE IL-13 RECEPTOR ALPHA 2.	27	143.5	6.9	425	11	Q9JM58
GN IL13RA2.	28	138	6.6	390	4	Q9UEH7
OS Mus musculus (Mouse).	29	135	6.5	346	13	O93404
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	30	130.5	6.3	198	6	O18985
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	31	126.5	6.1	329	4	Q9UQ41
OX NCBI_TaxID=10090;	32	119.5	5.7	371	4	Q9HC73
RN [1]	33	117.5	5.6	896	4	Q13594
RP SEQUENCE FROM N.A.	34	117.5	5.6	906	4	Q13593
RC STRAIN=C3H/HEJ; TISSUE=THYMUS;	35	117.5	5.6	958	4	Q13592
RX MEDLINE=98391042; PubMed=9725226;	36	116.5	5.6	1282	5	Q9VWE0
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,	37	114	5.5	894	6	Q9MYL1
RA Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,	38	114	5.5	925	6	Q9MYK9
RA Collins M.;	39	114	5.5	1163	6	Q9MYL2
RT The murine IL-13 receptor alpha 2: molecular cloning,	40	114	5.5	1194	6	Q9MYL0
RT characterization, and comparison with murine IL-13 receptor alpha 1.;	41	113.5	5.4	896	4	Q92919
RL J. Immunol. 161:2317-2324(1998).	42	113.5	5.4	958	4	Q92920
DR EMBL; U65747; AAC33240.1; .	43	113.5	5.4	1165	4	Q92921
DR MGD; MGI:1277954; IL13ra2.	44	111	5.3	628	11	Q9JKG1
DR InterPro; IPR002996; .	45	110	5.3	6875	6	Q28733
DR InterPro; IPR003532; .						
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN.1.						
SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;						

Query Match 57.2%; Score 1194.5; DB 11; Length 383;

Best Local Similarity 58.9%; Pred. No. 1.3e-98;

Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

QY 1 MAFVCLAIGCLYELISTTFGTGSSSTDEIKVNPQDFEIVDPGVLGYLVQWPPPLSLD 60

Db 1 MAFV-HIRCLCILLCTITGYS-----LEIKVNPQDFEILDPLGLLYLVQWPPPVIE 54

QY 61 HFKECTVEYELKYNIGSETWTKITITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120

Db 55 KFGGCTLEYELKYNVDSDSKITITRNLIYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQ 114


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FT NON_TER 349 349
SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 12.7%; Score 264.5; DB 6; Length 349;
Best Local Similarity 24.4%; Pred. No. 1.2e-15;
Matches 83; Conservative 63; Mismatches 135; Indels 59; Gaps 16;

QY 53 WOPPLSLDHFKEVEYELKYRNTGSETWKTITKNLHYKDGFDLNLKGIEAKIHTLLPWQ 112
Db 18 WNPPEGAS--PNCISLKY---FSGNGKQDKKIAPET-HRSKEVPLNERICLQVGS-----Q 67

QY 113 C-TNGSEVQSSWAEITTYWISQGPETKQVDMDCVYNNWQYLLCSKPGIGVLDITNYL 171
Db 68 CSTNESEKPSILVEKCF-SPEGDPESAVTALQCIWHLNRYMKCTWLPGRNASDPNVL 126

QY 172 FYWTEGLDHALQVDYIKADGONTGCRFPYLEASD--YKDFYICVNGSSSENKPIRSYFT 229
Db 127 YWHSNLGKILQCNFYR-EGQHIACSFNLTKVKDSSFQHSQVQVMDRDNAGKISPSFNI 185

QY 230 FOLQNIKVPPLPPVLTFTRESSCEIKLKWISPLGPIPARCFDYIEIREDDTTTLVTATVE 289
Db 186 VPLSHVKP-DPSHIKNLSFONGDLYQWNTPNQ-NFOSQCLCYEVEVINSHA----- 235

QY 290 NETYLTNTNTR-----QLCFVV-----RSKVNIYC-SDDGIWS 323
Db 236 -ETHDIFVEEAKQNTQEFEGNLEGTCFCFVMPVGLPDLTNTVRIRVKTNKLCEYEDDKLWS 294

QY 324 EWSDKQCEGEDLSKKYLLRFLWLPFGILLIVIEVTGLLL 363
Db 295 NWS-----QAMSIGOKANQTFYIT--TLLIIPVIVAAVI 327

RESULT 7
Q9UDY5 PRELIMINARY; PRT; 279 AA.
AC Q9UDY5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81380; RAD00511.2; -.
DR HSP; P40189; I8QU.
DR InterPro; IPR002996; -.
DR InterPro; IPR003532; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 279 AA; 31658 MW; E74141FE9F8E9EBB CRC64;

Query Match 11.6%; Score 241.5; DB 4; Length 279;
Best Local Similarity 27.7%; Pred. No. 1e-13;
Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;

QY 11 LYTFELISTFGCTSSDTEIKVNPQDFEIVDPGYLXLQWQPPSLSDHFKECTVEY- 69
Db 10 LWALLCAGGSGGGGGAAPTQPPVTNLSVSVENLCTVIWNPPEGAS--SNCSLWYF 67

QY 70 ----ELKYRIGSTWKTITKNLHYKDGFDLNLKGIEAKIHTLLPWQ--TNGSEVQSSWA 124
Db 68 SHFGDKQDKKIAPETRSI-----EVLPLNERICLQVGS-----QCSNESEKPSILV 114

QY 125 ETTTWIS-POGIPETKQVDMDCVYNNWQYLLCSKPGIGVLDITNYLFWYEGLDHALQ 183
Db 115 EKC--ISPPEGPESAVTELQCIWHLNLSYMKCSWLPGRNTPDNTNLTLYYHRSLEKIHQ 172
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QY 184 CVDYIKADGONIGCRFPYLEASD--YKDFYICVNGSSSENKPIRSYFTFOLQNIKVLPP 241
Db 173 C-ENIFREGQYFCGSFDTLTKVKDSSFQHSQVIMVKDNAGKIKPFSNIVPLTSRVKPDPP 231

QY 242 --VYLTFTRESSCEIKLKWISPLGPIPARCFDYIEIREDDT 281
Db 232 HIKNLSPHND---DLVYQWENPQNF-SRCLFYEVEVNNSTQ 269

RESULT 8
Q9DEQ1 PRELIMINARY; PRT; 363 AA.
AC Q9DEQ1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN SEQUENCE FROM N.A.
RA Wang T., Secombes C.J.;
RL "Cloning and expression of the first non-mammalian cytokine receptor
common gamma chain gene in rainbow trout (Oncorhynchus mykiss).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276623; CAC09429.1; -.
KW Receptor.
FT NON_TER
SQ SEQUENCE 363 AA; 41861 MW; DF69B2EBE3EAA06D3 CRC64;

Query Match 9.5%; Score 197.5; DB 13; Length 363;
Best Local Similarity 21.9%; Pred. No. 1.2e-09;
Matches 61; Conservative 56; Mismatches 134; Indels 27; Gaps 9;

QY 97 LNKGIEAKIHTLLPWQCTNGSEVQSSWAEITTYWISQGPETKQVDMDCVYNNWQYLLCS 156
Db 1 IHKVRVELVTIPTVIHFDMKMGWS--LFLISLOGYEAPSTPNVCLINDIYVNCI 58

QY 157 WKPGIGVLLDTNLYFYWTEGLDHALQVDYIKADGONIGCRFPYLEASDYKDFYICVNG 216
Db 59 WSE--QSIPEVNTFTFSRRIKDNMECTTYLQESYAVGCLSYDKSDRFR----- 108

QY 217 SSENKPIRSYFTFQ---LQNIKVPPLPPVLTFTRESSCEIKLKWISPLGPIPARCFDYE 273
Db 109 TLTKLVHQNMSYVQDHNLSKMKLYPPVNLSEVMNKDPELNLYNNNSKNFT---CIESE 165

QY 274 IEIREDDTTTLVTATVENE--TYTLKTTNETRQLCFVRSKVNIVGSDGIVSEWSDKQWE 332
Db 166 VRYRINSKWKTSPTSKEQYAVAFPLKSSRYEFOVARVNDMCGESEFWSEWSQIQWD 225

QY 333 G-----EDLSKTKLLRFWLP-FGFIILIVFVTGLLL 363
Db 226 SMKGNNTDISGS--MSVWKPVLSLVGTMTLFIACML 262

RESULT 9
Q9PT10 PRELIMINARY; PRT; 611 AA.
AC Q9PT10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE PROLACTIN RECEPTOR A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
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RN  SEQUENCE FROM N.A.
RX  MEDLINE=20087225; PubMed=10618394;
RT  Huang H., Brown D.D.;
RT  "Prolactin is not a juvenile hormone in xenopus laevis
RT  metamorphosis.";
RL  Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR  EMBL; AF193800; AAF05776.1; -
DR  HSP; P16471; IBP3.
DR  InterPro; IPR001777; -
DR  InterPro; IPR002996; -
DR  InterPro; IPR003528; -
DR  Pfam; PF00041; fn3; 1.
DR  SMART; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR  Receptor.
KW  Receptor.
SQ  SEQUENCE 611 AA; 68255 MW; 85629F917766FFB6 CRC64;

Query Match      8.9%; Score 185.5; DB 13; Length 611;
Best Local Similarity 28.3%; Pred. No. 2.7e-08;
Matches 71; Conservative 32; Mismatches 109; Indels 39; Gaps 11;

QY  127 TYWISPGIPETKVQDMCVYNNQYLCSWKPGIGVLLDYNLFWYEGLDHALQCV 186
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  22 TVSLNAQSLPGKPVID-KCRSEYKVTSCWKNKPGSDGLPTNYSLLYRKENDPKIY 80
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |

QY  187 YIKADGQNGICRFPYLEADSKDFYICVNGS-----SENKPIRSSYFTQLQNI 239
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db  81 YV-TSGLN-SCFFDKAHTSFWIFHYIYNATNALGSNVSDSESDVTY-----IV 131
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |

QY  240 PPVYLITFTRESS-CEIKLKWSIPLGPIPARCFD-----YEIEIREDDTTLV 289
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  132 PPTNVSLAVESGHDLKWK-----LPPAMVDVQSGWLTLYKYEVRYKEEQEWEAHLV 185
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |

QY  290 NETYTLKTTNETQLCFVVRSKVNIYCS-DDGIWSEWSDKOCWEGEDLSKTLRLFWLP 348
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  186 GNQLKLKLFGLTPGNGYVQ----VRCKPDSGHWSEWSTESYIQIPGGKKTDLTWISI 241
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |

QY  349 GFILLIVFVT 359
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db  242 G-ALSAVICLT 251
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 11
Q64146 PRELIMINARY; PRT; 896 AA.
AC Q64146;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
GN RIL-3R<BETA>.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370942; PubMed=7643220;
RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
RT microglia and its mRNA expression in vivo.";
RL J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-WISTAR; TISSUE=BRIN;
RA Gebicke-Haerter P.J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; S79263; AAB35068.1; -
DR EMBL; AJ000555; CAA04186.1; -
DR InterPro; IPR00282; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003531; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal.
FT NON_TER 1 896
FT NON_TER 896
SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

Query Match      8.5%; Score 178; DB 11; Length 896;
Best Local Similarity 21.4%; Pred. No. 2e-07;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY  5 CLAIGCL--YT-FLISTTFGCTSSDTEIKVN-----PPQDFEIVDPYGLYL 49
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  94 CVPRRCVLPYTFQSVSKEDYISLQDRDLISLHVPLAQHVQPPPPKDISPSG--DHF 151
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |

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RN  SEQUENCE FROM N.A.
RX  MEDLINE=20087225; PubMed=10618394;
RT  Huang H., Brown D.D.;
RT  "Prolactin is not a juvenile hormone in xenopus laevis
RT  metamorphosis.";
RL  Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR  EMBL; AF193800; AAF05776.1; -
DR  HSP; P16471; IBP3.
DR  InterPro; IPR001777; -
DR  InterPro; IPR002996; -
DR  InterPro; IPR003528; -
DR  Pfam; PF00041; fn3; 1.
DR  SMART; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR  Receptor.
KW  Receptor.
SQ  SEQUENCE 611 AA; 68255 MW; 85629F917766FFB6 CRC64;

Query Match      8.9%; Score 185.5; DB 13; Length 611;
Best Local Similarity 28.3%; Pred. No. 2.7e-08;
Matches 71; Conservative 32; Mismatches 109; Indels 39; Gaps 11;

QY  127 TYWISPGIPETKVQDMCVYNNQYLCSWKPGIGVLLDYNLFWYEGLDHALQCV 186
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  22 TVSLNAQSLPGKPVID-KCRSEYKVTSCWKNKPGSDGLPTNYSLLYRKENDPKIY 80
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |

QY  187 YIKADGQNGICRFPYLEADSKDFYICVNGS-----SENKPIRSSYFTQLQNI 239
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db  81 YV-TSGLN-SCFFDKAHTSFWIFHYIYNATNALGSNVSDSESDVTY-----IV 131
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |

QY  240 PPVYLITFTRESS-CEIKLKWSIPLGPIPARCFD-----YEIEIREDDTTLV 289
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  132 PPTNVSLAVESGHDLKWK-----LPPAMVDVQSGWLTLYKYEVRYKEEQEWEAHLV 185
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |

QY  290 NETYTLKTTNETQLCFVVRSKVNIYCS-DDGIWSEWSDKOCWEGEDLSKTLRLFWLP 348
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db  186 GNQLKLKLFGLTPGNGYVQ----VRCKPDSGHWSEWSTESYIQIPGGKKTDLTWISI 241
    | : : | : | : | : | : | : | : | : | : | : | : | : | : |

QY  349 GFILLIVFVT 359
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db  242 G-ALSAVICLT 251
    | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 10
Q9IBF6 PRELIMINARY; PRT; 611 AA.
AC Q9IBF6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;
RT "Cloning of a cDNA for xenopus prolactin receptor and its
RT metamorphic expression profile.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030443; BAA90400.1; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68315 MW; 7E0DF76F21D8CE97 CRC64;

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:05:53 ; Search time 60.7 Seconds
(without alignments)
379.524 Million cell updates/sec

Title: US-09-077-817-2

Perfect score: 2104

Sequence: 1 MAVFVLAIGCLYFLISTTF.....LLLRKPNTYPKMIPFFCDT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2104	100.0	380	AAW24972	Human interleukin-
2	2104	100.0	380	AAW35295	Human IL-13 bindin
3	2104	100.0	380	AAW36613	Human Zcytor2 cyto
4	2104	100.0	380	AAW41520	Human HR-1 recepto
5	2104	100.0	380	AAW41502	Human cytokine/pep
6	2104	100.0	380	AAW33603	Homo sapiens HR-1
7	2104	100.0	380	AAW35296	IL-13 binding chai
8	2104	100.0	380	AAW72136	Human interleukin
9	2104	100.0	380	AAW29748	Human IL-13 recept
10	2078	98.8	380	AAW36614	Human Zcytor2 cyto
11	1853	88.1	372	AAW36616	Celebus macaque Zc

12	1753	83.3	315	19	AAW56261	Mature interleukin
13	1753	83.3	359	19	AAW56260	Construct containi
14	1194.5	56.8	383	18	AAW35294	Murine IL-13 bindi
15	1194.5	56.8	383	21	AAW52595	IL-13 binding chai
16	1194.5	56.8	383	22	AAW72135	Murine interleukin
17	1194.5	56.8	383	22	AAW29747	Mouse IL-13 recept
18	456	21.7	157	19	AAW56252	Interleukin-13 bin
19	311.5	14.8	396	13	AAW22216	Sequence of human
20	311.5	14.8	396	13	AAW22220	Sequence of secret
21	311.5	14.8	420	13	AAW22219	Human interleukin-
22	311.5	14.8	420	13	AAW82842	Human IL-5 recepto
23	310.5	14.8	421	13	AAW22504	Sequence of human
24	305.5	14.5	420	13	AAW22215	Protein used in pr
25	297	14.1	313	18	AAW21856	Mouse interleukin-
26	296	14.1	426	18	AAW09821	Human interleukin-
27	295.5	14.0	427	18	AAW24973	Human interleukin-
28	295.5	14.0	427	22	AAW19807	Human interleukin-
29	294.5	14.0	426	18	AAW09822	IL5-R-GBP 130 fusi
30	292.5	13.9	1026	16	AAW70121	Soluble human IL-5
31	292	13.9	335	13	AAW25063	shIL-5R-alpha. Sy
32	292	13.9	335	14	AAW33699	Human interleukin-
33	286.5	13.6	427	22	AAW19808	IL-13/IL-4 dual tr
34	285	13.5	793	21	AAW22208	IL-13/IL-4 dual tr
35	249.5	11.9	155	19	AAW56255	Sequence of interl
36	248	11.8	398	13	AAW22212	Sequence of interl
37	247	11.7	415	13	AAW22211	Sequence of interl
38	247	11.7	415	13	AAW22217	Sequence of interl
39	229	10.9	332	13	AAW22214	Sequence of interl
40	229	10.9	332	13	AAW22213	Sequence of interl
41	229	10.9	332	13	AAW22218	IL-2 receptor gamm
42	229	10.5	369	15	AAW47148	IL-2 receptor gamm
43	220	10.4	347	15	AAW47149	Murine IL-2R gamma
44	219	10.4	369	15	AAW59094	
45	209.5	10.0	369	15	AAW59094	

ALIGNMENTS

RESULT 1

AAW24972 ID AAW24972 standard; protein; 380 AA.

XX AC AAW24972;

XX 22-JUN-1998 (first entry)

DT Human interleukin-13 beta receptor.

DE Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.

XX Homo sapiens.

XX WO9720926-A1.

XX 12-JUN-1997.

XX 07-NOV-1996; 96WO-FR01756.

XX 06-DEC-1995; 95FR-0014424.

XX (SNFI) SANOFI SA.

XX Caput D, Ferrara P, Laurent P, Vita N;

XX WPI; 1997-319773/29.

XX N-PSDB; AAT85826, AAT86464.

XX New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allergy, etc

XX Claim 1; Figure 2a; 83pp; French.

XX This sequence represents interleukin-13 (IL-13) beta receptor. The
 CC invention relates to new purified peptides comprising 380 or 427 amino
 CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
 CC affinity, but acquires high affinity when associated with the IL-4
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies
 CC such as loss of heterozygosity and rearrangements, or chromosomal
 CC anomalies. They are also used for production of recombinant IL-13R beta
 CC and alpha which can be used as IL-13 antagonists, specifically to
 CC regulate IL-13-induced responses for treatment of inflammation and
 CC allergy. IL-13 receptors are also useful as antisense molecules for gene
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
 CC immuncassays) to diagnose diseases associated with abnormal expression
 CC of IL-13 receptors; when coupled to a toxin also for treatment of
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are
 CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
 CC is encoded by the nucleic acid sequence shown in Figure 2a in the
 CC specification (AAT86464), which is not the same as that shown in the
 CC sequence listing (AAT85828).
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPDPQDFEIVDPGLGYLYLQWPPPLSLD 60
 Db 1 mafvclaigcltyflstftgctssdteikvnpdpqdfvdpqlylylqwpplsl 60

Qy 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkynigsetwktitknlnhykdgfdlnkgleakihltllpwqctngse 120

Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNWQYILCSWKPGIGVLLDTNLYNLFYWEGLDH 180
 Db 121 sswaettywispgipetkvdmdcvynnwqyilcswkpgigvlltdtnnlyfywegldh 180

Qy 181 ALOQVDYIKADQNGICRFPYLEASDKDFYICVNGSENKPIRSSYFTFOLQIVRPLP 240
 Db 181 alqcvdyikadqngicrfyleasdkdfyicvngsenkpirssyftfqlqivrpplp 240

Qy 241 PVLFTFRESSCEKILWSIPGLPIPARCFDYEIEIREDDTTLVTAVENETYILKTNE 300
 Db 241 pvyitfressceiklwsipglpigarcfdyeiieireddtllvtatvenetyilktne 300

Qy 301 TROLCFVVRKVNLYCSDGGLWSWSBKQWGEDLSKTLLEWLPFGFTLLILVIFVTG 360
 Db 301 trqlcfvvrkvnlycsdggllwswsbkqwedlskttlrlwlpfgftllilvifvtg 360

Qy 361 LLRLKNTYKMPIEFFCDT 380
 Db 361 llrlkntypkmpieffcdt 380

RESULT 2
 AAW35295
 ID AAW35295 standard; Protein; 380 AA.

XX AAW35295;

XX 27-MAR-1998 (first entry)

XX Human IL-13 binding chain of the IL-13 receptor.

XX Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.

XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..25
 FT /label= signal_sequence
 FT /note= "putative"
 FT Protein 26..380
 FT /label= mature_protein
 FT Domain 26..341
 FT /label= extracellular_domain
 FT Domain 342..362
 FT /label= transmembrane_domain
 FT Domain 363..380
 FT /label= intracellular_domain

XX WO9731946-A1.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-US03124.

XX 01-MAR-1996; 96US-0609572.

XX (GEMY) GENETICS INST INC.

XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;

XX WPI; 1997-448632/41.

DR N-PSDB; AAT95214.

XX New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transformed cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis

XX Claim 11; Pages 34-35; 49pp; English.

XX The present sequence represents the human interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied,
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.

XX Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 18; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLFTSTFCTSSDTEIKVNPDPQDFEIVDPGLGYLYLQWPPPLSLD 60

Db 1 mafvclaigcltyflstftgctssdteikvnpdpqdfvdpqlylylqwpplsl 60

Qy 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120

Db 61 hfkectveyelkynigsetwktitknlnhykdgfdlnkgleakihltllpwqctngse 120

Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNWQYILCSWKPGIGVLLDTNLYNLFYWEGLDH 180

Db 121 sswaettywispgipetkvdmdcvynnwqyilcswkpgigvlltdtnnlyfywegldh 180

QY 181 ALQCVYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQLOINIVKPLP 240
Db 181 alqcvdyikadqngicrfyleasdykdfyicvngsenkpirssyftfqlqnvkplp 240
QY 241 PVYLTFTRESSCEIKLWSIPGLPIPARCFDYETIREDDTTLVTAIVENETYTLKTTNE 300
Db 241 pvyltftressceiklwsipglpmparcdyeteireddttlvatvenetytlktne 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQWEGEDLSKTLRLFWLPFGFTLILVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewsdkqwegedlsktlrlfwlpfgftlilvifvtg 360
QY 361 LLLRKPNTPYKMIPEFFCDT 380
Db 361 lllrkpntpykmipecfcdt 380

RESULT 3
AAW36613
ID AAW36613 standard; Protein; 380 AA.
XX AAW36613;
XX AC
XX DT 30-MAR-1998 (first entry)
XX DE Human Zcytor2 cytokine receptor protein.
XX KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
XX KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 340..363
XX FT /label= transmembrane_domain
XX FT Domain 364..380
XX FT /label= intracellular_domain
XX FT Domain 25..339
XX FT /label= ligand_binding_domain
XX PN WO9733913-A1.
XX PD 18-SEP-1997.
XX PF 12-MAR-1997; 97WO-US04043.
XX PR 13-MAR-1996; 96US-0013345.
XX PA (ZYMO) ZYMOGENETICS INC.
XX BA Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
XX PI O'Hara PJ;
XX DR WPI; 1997-470820/43.
XX DR N-PSDB; AAT96782.
XX PT New nucleic acid encoding testis-specific cytokine receptor - useful
XX PT for identification of ligands or antagonists, potentially for use as
XX PT male contraceptives or for infertility treatment
XX PS Claim 2; Page 47-48; 79pp; English.
XX CC This sequence represents a novel ligand-binding receptor, Zcytor2,
XX CC which shares homology with cytokine receptors and was isolated from human
XX CC placental polyA+ RNA. The resulting polypeptide is a receptor for
XX CC cytokines (particularly interleukin-13) and is expressed on the surface
XX CC of testicular cells, probably being involved in spermatogenesis. It can
XX CC be used to detect ligands that promote proliferation and/or
XX CC differentiation of such cells in cultures and may also be used to treat
XX CC infertility. Antagonists of this receptor may be used to characterise
XX CC ligand-receptor interactions and as male-specific contraceptives. By
XX CC blocking the action of IL-13, receptor antagonists and ligand-binding
XX CC this receptor can also be used to modulate immune function, e.g. in

CC allergy and asthma, as a diagnostic to determine circulating levels of
CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.
XX SQ Sequence 380 AA;
Query Match 100.0%; Score 2104; DB 18; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.2e-198;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIGCLYTFELISTTFTCTSSDTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
Db 1 mafvclaigcltyflisttftctssdteikvnpqdfeidvpgilylylwqppisld 60
QY 61 HFKECTVEYELKYRNIGSETWKTITTNLHYKDFDNLKGIKIEAKIHLLPWQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwktitknlhykdgfdnlkgieakihtllpwqctngsevg 120
QY 121 SSWAETTYWISPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
Db 121 sswaettywispgipetkvqdmcdvynnwqyllcswkpgigvlldtnynlfywegldh 180
QY 181 ALQCVYIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQLOINIVKPLP 240
Db 181 alqcvdyikadqngicrfyleasdykdfyicvngsenkpirssyftfqlqnvkplp 240
QY 241 PVYLTFTRESSCEIKLWSIPGLPIPARCFDYETIREDDTTLVTAIVENETYTLKTTNE 300
Db 241 pvyltftressceiklwsipglpmparcdyeteireddttlvatvenetytlktne 300
QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQWEGEDLSKTLRLFWLPFGFTLILVIFVTG 360
Db 301 trqlcfvvrskvniycsddgiwsewsdkqwegedlsktlrlfwlpfgftlilvifvtg 360
QY 361 LLLRKPNTPYKMIPEFFCDT 380
Db 361 lllrkpntpykmipecfcdt 380

RESULT 4
AAW41520
ID AAW41520 standard; Protein; 380 AA.
XX AAW41520;
XX AC AAW41520;
XX DT 22-JUN-1998 (first entry)
XX DE Human HR-1 receptor.
XX KW HR-1 receptor; human; cytokine; infection; asthma; allergy;
XX KW haematopoietic disorder; tumour; therapy; diagnosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT /label= Sig_peptide
XX FT Protein 22..380
XX FT /label= Mat_protein
XX PN WO9747741-A1.
XX PD 18-DEC-1997.
XX PF 12-JUN-1996; 96WO-US10262.
XX PR 12-JUN-1996; 96WO-US10262.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Appelbaum ER, Hu J;
KW WPI: 1998-052308/05.
DR N-PSDB: AAV04131.
XX Nucleic acid sequence encoding human cytokine peptide hormone
PT receptor - useful to treat, prevent or diagnose, e.g. lowered
PT resistance to infection, asthma, allergy or haematopoietic disease
XX Claim 13; Page 62-64; 76pp; English.
XX This protein comprises a novel human cytokine/peptide hormone
CC receptor, designated the HR-1 receptor, that shows 27% identity
CC and 52% similarity to the interleukin-5 receptor. Its amino acid
CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
CC human testis library. Recombinant HR-1 receptor can be expressed
CC in claimed host cells, and used in a claimed method for identifying
CC compounds which bind to, and activate or inhibit, it. HR-1
CC receptor activators and agonists can be used to treat, prevent or
CC diagnose predisposition to lowered resistance to infection, asthma,
CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
CC aplastic anaemia, neutropaenia or cytotoxic treatments for cancer.
CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
CC be used to treat conditions associated with HR-1 receptor
CC overexpression. The antibodies can also be used to determine HR-1
CC receptor levels, since overexpression may be diagnostic of tumours.
XX Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.2e-198;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFVCLAIGCLYTLISTTFCGTSSTTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
Db 1 mafvclaigcllytlsttfgctssstteikvnpqdfelvdpgylglylqwqpplsl 60
Qy 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNKGEAKIHLPLPWQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwktitknlnhykdgfdlnkgeakihlplwqctngse 120
Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
Db 121 sswaettywispogipetkvdmdcvynnwqyllcswkpgigvlldtnlnlyfwe 180
Qy 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSYFTFOLQNVKPLP 240
Db 181 alqcvdyikadqngicrfpyleasdykdfyicvngssenkpirsyftfqlqnvkpl 240
Qy 241 PVYLTFRESSECEIKLWSIPGLPIPARCFDYEIEIREDDTTLVTAVENTYTLKTNE 300
Db 241 pvytlfresseceiklwsipglpigarcfdyeieireddtlvtavenetytlktne 300
Qy 301 TRQLCFVVRKVNIVYCSDDGIWSWSKQWEGEDLSKKTLLRFLWLPFGFLLILVIFVTG 360
Db 301 trqlcfvvrkvnivycsddgiwswsdkqwegedlskktllrflwlpfgfllilvif 360
Qy 361 LLLRKNPTNPKMPEFFCDT 380
Db 361 lllrkpnptypkmpfeffcdt 380

RESULT 5
AAW41502
ID AAW41502 standard; Protein; 380 AA.
XX
AC AAW41502;
XX
DT 08-JUN-1998 (first entry)
XX Human cytokine/peptide receptor, HR-1 receptor.

XX
KW HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
KW neutropaenia; therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1..21
FT Peptide /label= Sig_peptide
FT Protein 22..380
FT /label= Mat_protein
FT /note= "Claim 14"
XX EP812913-A2.
XX 17-DEC-1997.
XX 04-JUN-1997; 97EP-0303815.
XX 12-JUN-1996; 96US-0017843.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Appelbaum ER, Hu J;
XX WPI: 1998-034974/04.
XX N-PSDB: AAV04075.
XX Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
PT increase resistance to infections in individuals with trauma and/or
PT burns
XX Claim 13; Page 27-28; 34pp; English.

XX This protein comprises a novel human cytokine/peptide hormone
CC receptor, designated HR-1 receptor. The amino acid sequence
CC was deduced from a cDNA clone (see AAV04075) isolated from a human
CC testis cDNA library. It shows 27% amino acid identity and 52%
CC similarity with the human interleukin-5 receptor. Also claimed are
CC polynucleotides encoding HR-1 receptor, vector and host cells, an
CC antagonist to the polypeptide, antibody against the polypeptide, an
CC antagonist that inhibits the activity of the polypeptide, a process
CC for diagnosing a disease, or a susceptibility to disease, related
CC to expression of HR-1 receptor, and a method for identifying
CC compounds that activate or inhibit the HR-1 receptor. HR-1
CC receptor protein and polynucleotides can be used for research,
CC biological, diagnosis and (gene) therapy applications, e.g. to
CC increase resistance to infections in individuals with trauma and/or
CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
CC predisposition to asthma, allergic disorders or disorders of
CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
CC cyclic neutropaenia or as a consequence of cytotoxic therapy of
CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.
XX Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.2e-198;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAFVCLAIGCLYTLISTTFCGTSSTTEIKVNPQDFEIVDPGILGYLYLQWQPPLSLD 60
Db 1 mafvclaigcllytlsttfgctssstteikvnpqdfelvdpgylglylqwqpplsl 60
Qy 61 HFKECTVEYELKYNIGSETWKTITKNLHYKDGFDLNKGEAKIHLPLPWQCTNGSEVQ 120
Db 61 hfkectveyelkynigsetwktitknlnhykdgfdlnkgeakihlplwqctngse 120
Qy 121 SSWAETTYWISPOGIPETKVDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
Db 121 sswaettywispogipetkvdmdcvynnwqyllcswkpgigvlldtnlnlyfwe 180

Db 121 sswaettywispagipetkvqmdcvynwqyllcswkpgigvlltdnynlfwyegldh 180
 QY 181 ALOCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLQNIYKPLP 240
 Db 181 alqcvdyikadgqncigrfyleasdykdfyicvngsssenkpirssyftfqlqniykvlp 240
 QY 241 PVYLTFTRESSCEIKLWKSIPGLPIPARCFDYEIEIREDDTTLVATVENETYLKTTNE 300
 Db 241 pvytlftressceiklwksiplgpiarpcfdeyleireddttlvatvenetylktne 300
 QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGEDLSKTLRLFWLPFGFILLIIVFVTG 360
 Db 301 trqlcfvvrskvniycsddgiwsewsdkqcegedlskllrlfwlpfgfillilvifvtg 360
 QY 361 LLRKPNTPYKMIPEFFCDT 380
 Db 361 llirkpntypkmipecfdt 380

RESULT 6
 AAW33603
 ID AAW33603 standard; Protein; 380 AA.
 AC AAW33603;
 XX
 XX 08-JUN-1998 (first entry)
 DT Homo sapiens HR-1 receptor.
 DE
 XX Cytokine; hormone receptor; AIDS; acquired immune deficiency;
 KW syndrome; aplastic anaemia; neutropaenia; cancer treatment;
 KW infection resistance; diagnosis; tumours; HR-1 receptor;
 KW asthma; allergic; haematopoietic; disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "signal peptide"
 XX
 XX W09747742-A1.
 XX 18-DEC-1997.
 XX
 XX 09-JUL-1996; 96WO-US11459.
 XX
 XX 12-JUN-1996; 96WO-US10262.
 PR 12-JUN-1996; 96US-0017843.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA Appelbaum ER, Hu J;
 XX
 DR WPI; 1998-052309/05.
 DR N-PSDB; AAV02295.
 XX
 XX DNA encoding human cytokine-peptide hormone receptor - useful for
 PT treating preventing or diagnosing, e.g. lowered resistance to
 PT infection, asthma, allergy, or haematopoietic disease
 XX
 XX Claim 15; Fig 1; 75pp; English.
 XX
 CC The sequence is that of the human cytokine/peptide hormone receptor
 CC (HR-1 receptor). This, or it's activators or agonists, can be used to
 CC treat, prevent or diagnose predisposition to lowered resistance to
 CC infection, asthma, allergic or haematopoietic disorders, e.g. where
 CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
 CC neutropaenia or cytotoxic treatments for cancer. Antagonists of the
 CC receptor, e.g. antibodies or fragments of it may be used to treat
 CC conditions associated with overexpression of the HR-1 receptor, e.g.
 CC those listed above. Antibodies may also be used to assay levels of HR-1
 CC receptor, overexpression of which may be diagnostic of tumours, by usual

CC immunoassays; to isolate and identify HR-1 receptor-expressing cells; or
 CC for affinity purification of the HR-1 receptor.

SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 19; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYFLISTTFTGCTSSDTEIKVNPQDFEIVDPGILGYLYLQWOPPLSLD 60
 Db 1 marvclaiagcllyflisttftgctssdteikvnpqqdfelvdp9ylylylqwppplsl 60
 QY 61 HFKECTVEYELKYRNIGSETWKTIIITKNLHYKDGFDLNKGIEAKIHFTLLPWQCTNGSEVQ 120
 Db 61 hfkectveyelkyrnigsetwktitknlykdgfdlnkgleakihtllpwqctngsevg 120
 QY 121 SSWAETTYWISPOGIPETKVQMDCVYNNQYLLCSWKPGIGVLLDTNYNLFYWEGLDH 180
 Db 121 sswaettywispqgipetkvqmdcvynwqyllcswkpgigvlltdnynlfwyegldh 180
 QY 181 ALOCVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLQNIYKPLP 240
 Db 181 alqcvdyikadgqncigrfyleasdykdfyicvngsssenkpirssyftfqlqniykvlp 240
 QY 241 PVYLTFTRESSCEIKLWKSIPGLPIPARCFDYEIEIREDDTTLVATVENETYLKTTNE 300
 Db 241 pvytlftressceiklwksiplgpiarpcfdeyleireddttlvatvenetylktne 300
 QY 301 TROLCFVVRSKVNIYCSDDGIWSEWSKQCEGEDLSKTLRLFWLPFGFILLIIVFVTG 360
 Db 301 trqlcfvvrskvniycsddgiwsewsdkqcegedlskllrlfwlpfgfillilvifvtg 360
 QY 361 LLRKPNTPYKMIPEFFCDT 380
 Db 361 llirkpntypkmipecfdt 380

RESULT 7

AA95296
 ID AA95296 standard; Protein; 380 AA.

XX
 AC AA95296;

XX 12-SEP-2000 (first entry)

DE IL-13 binding chain of human IL-13 receptor.

XX Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
 KW cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
 KW immune complex disease; lupus; nephritis; thyroiditis;
 KW Grave's disease; inflammatory; infection; therapy; anti-allergic;
 KW anti-inflammatory; antiasthmatic; vaccine.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..25 "signal peptide"
 FT /note= "mature protein"
 FT 26..380
 FT 26..341
 FT /note= "extracellular domain; a polypeptide
 FT comprising amino acids 22-334 is
 FT specifically claimed in Claim 11(e)"
 FT 342..362
 FT /note= "transmembrane domain"
 FT 363..380
 FT /note= "intracellular domain; a polypeptide
 FT comprising amino acids 257-383 is
 FT specifically claimed in Claim 11(f)"
 XX

PN WO200036103-A1.
XX 22-JUN-2000.
XX 13-DEC-1999; 99WO-US29493.
XX 14-DEC-1998; 98US-0211335.
XX (GEMY) GENETICS INST INC.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
PI Wills-Karp M;
XX WPI: 2000-431587/37.
XX N-PSDB; AAA27912.
XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
PT an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
PT asthma, Grave's disease and inflammatory conditions of the lung -
XX Claim 11(d); Page 53-54; 60pp; English.
XX The present sequence is that of the interleukin-13 binding chain
CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated
CC human testis cDNA clone (see AAA27912). IL-13bc is a member of
CC the haematopoietin receptor family that acts as a mediator of
CC IL-13. The invention provides methods for the recombinant
CC production of IL-13bc polypeptides, including claimed full-length
CC IL-13bc, its extracellular domain, and its intracellular domain.
CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
CC of IL-13 and its receptor) can be used to treat conditions in
CC which IL-13 is implicated, particularly IgE-mediated conditions and
CC diseases including atopy, allergy, asthma, immune complex diseases
CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
CC thyroiditis and Grave's disease), lung inflammation,
CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
CC activation, IL-13bc proteins can also be used to enhance macrophage
CC activation, e.g. in vaccination, treatment of mycobacterial or
CC intracellular organisms or parasite infections. IL-13bc proteins
CC may also be used to potentiate the effects of IL-13 in vitro and
CC in vivo, as diagnostic agents, and to screen for agents capable of
CC binding to IL-13bc or IL-13 receptor, or which interfere with the
CC binding of IL-13 to its receptor.
XX
XX SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 21; Length 380;
Best Local Similarity 100.0%; Pred. No. 6.2e-198;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYFLISTTTCGCTSSSTTEIKVNPQDFEIVDPGGLYLYLQWQPLSLD 60
Db 1 mafvclaigcllyflisttfgctssstteikvnpqdfelvdpqgllylylqwpplsl 60

QY 61 HFKECTVEYELKYNIGSEWTKLITKNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120
Db 61 hfkectveyelkynigsewtklittknlyhkdgfdlنگkieakihltllpqwctngsevq 120

QY 121 SSWAETTYWISPGQIPETKVDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDH 180
Db 121 sswaettywispqgipetkvdmdcvynnyqyllcswkpgigvlltdntnlyfywegl 180

QY 181 ALQCDVYIKADGQNGICRFRPYLEADSKDYICVNGSSSENKPIRSSYFTFQQLNIVKPLP 240
Db 181 alqcdvyikadgqngicrfpyleadskdyfcvngsssenkpirssyftfqlnkvkpl 240

QY 241 PVIYTFRESSCEKIKWSIPLGPIPARCFDYEIREDDTTLVTATVENETYLKTNE 300
Db 241 pviytfressceikikwsiplgpiarpcfdyeirreddttlvtatvenetylktne 300

QY 301 TROLCFVVRKVNICYSDDGISWSESDKQWEGEDLSKKTLLRFLWLPFGFLLIVFVWG 360
Db 301 trqlcfvvrskvniycsddgiwsewskqwedlskktllrflwlpfgfllivirvtg 360

QY 361 LLDRKPNITYPKMIPEFFCDT 380
Db 361 llldrknptypkmipecfcdt 380

RESULT 8
AA72136
ID AAY72136 standard; Protein; 380 AA.
XX
XX AC AAY72136;
XX DT 24-APR-2001 (first entry)
XX Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
DE Human; IL-13: interleukin-13 binding chain of IL-13 receptor; IL13bc;
XX therapy; tissue fibrosis; Schistosoma infection; surgical incision;
KW cyostatic; wound; IL-13 related condition; allergic condition;
KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;
KW macrophage activation.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..25 /label= Signal_peptide
FT Region 1..81 /note= "This region is identical to the translated
FT sequence of an expressed sequence tag (EST) identified
FT as Y999f10.r1 human cDNA clone 41648 5"
FT Protein 26..380 /label= Mature_human_interleukin (IL)-13_binding_chain_
FT of_IL-13_receptor
FT Domain 26..341 /note= "Extracellular domain; this region is specifically
FT claimed in claims 1e, 6e, 15e and 23e"
FT Domain 342..362 /note= "Transmembrane domain"
FT Domain 363..380 /note= "Intracellular domain; this region is specifically
FT claimed in claims 1f, 6f, 15f and 23f"
XX
XX PN WO200078336-A1.
XX 28-DEC-2000.
XX 21-JUN-2000; 2000WO-US17103.
XX 21-JUN-1999; 99US-0334512.
XX (GEMY) GENETICS INST INC.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
PI Wills-Karp M;
XX WPI: 2001-080753/09.
XX N-PSDB; AAD02335.
XX Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis
PT in a mammalian subject, involves administering a pharmaceutical
PT composition comprising IL-13 antagonist -
XX
XX Claim 1a; Page 69-70; 72pp; English.
XX The invention relates to a method of treating, or inhibiting
CC the formation of tissue fibrosis in mammals, which involves
CC administering a pharmaceutical composition comprising interleukin
CC (IL)-13 antagonist. The protein of the invention is useful for

CC treating tissue fibrosis resulting from infection with Schistosoma
 CC or from healing of a wound which is a surgical incision, or
 CC inhibiting formation of tissue fibrosis which affects tissues such
 CC as liver, skin epidermis and endodermis, muscle, tendon, cartilage,
 CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
 CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,
 CC biliary tract and gut. It is also used in the treatment or modulation
 CC of various IL-13 related conditions such as allergic conditions,
 CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.
 CC The present sequence is human interleukin (IL)-13
 CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used
 CC to potentiate the effects of IL-13. This protein is also used to
 CC enhance macrophage activation and hence can be used in vaccination
 CC or treatment of mycobacterial or parasitic infections.
 CC
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLATGCLYTLFISTFGCTSSDPEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
 DB 1 mafvclaigclytlfistfgctssdteikvnpqdfelvdpgylgylylqwgppslsld 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNKGIKTEAKHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkyrnigsetwktitknhykdgfdlnkgeakhtllpwqctngsevg 120
 QY 121 SSWAETTYWISPGIPETPKVQDMDCVYNNWOYLCSWKPGIGVLDTNLYNFYWEGLDH 180
 DB 121 sswaettywispggipetkvdqmdcvynwqyllycswkpgigvlltdnynlfywegldh 180
 QY 181 ALQCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQOLNIVKPLP 240
 DB 181 alqcvdyikadgqngicrfpyleasdykdfyicvngssenkprrssytfqlqnvkplp 240
 QY 241 PVYLTFRESSCEIKLWSIPLGPIPARCFDYEIEIRDDDTLVATVENETYTLKTNE 300
 DB 241 pvyiltfressceiklwsiplgpiparcfdyeyeierrddtlvtatvenetytlktne 300
 QY 301 TRQICFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
 DB 301 trqicfvvrskvniycsddgiwsewskqwedlskktllrflwlpfgfillilvifvtg 360
 QY 361 LLRKPNTPYKMWIPEFFCDT 380
 DB 361 llrkpntypkmipecfcdt 380

RESULT 9
 AAB29748
 ID AAB29748 standard; Protein; 380 AA.
 XX
 AC AAB29748;
 XX
 XX
 XX 23-FEB-2001 (first entry)
 XX
 DE Human IL-13 receptor IL-13 binding chain (IL-13bc).
 XX
 KW Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
 KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnery;
 KW wound healing; schistosoma infection; liver; skin; muscle;
 KW cartilage; cardiac tissue; lung tissue; uterine tissue;
 KW intestinal tissue; vascular tissue; neural tissue.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO200006494-A1.
 XX
 XX
 PD 02-NOV-2000.
 XX

PF 28-APR-2000; 2000WO-US11612.
 XX
 PR 28-APR-1999; 99US-0301808.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 XX Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;
 PI Whitters MJ, Wood C;
 XX
 XX WPI: 2001-024676/03.
 DR N-PSDB; AAC81416.
 DR
 PT Treating or inhibiting tissue fibrosis resulting from infection with
 PT schistosoma and wound healing involves administering interleukin-13 or
 PT interleukin-4 antagonist
 XX
 PS Claim 1; Page 76-77; 82pp; English.
 XX

CC The invention relates to a method of treating fibrosis in a mammal
 CC by administering an interleukin-13 (IL-13) antagonist or an IL-4
 CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding
 CC chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or
 CC soluble fragments thereof. The method is useful for treating or
 CC inhibiting the formation of tissue fibrosis resulting from the healing
 CC of a wound, including a surgical incision wound, or from infection with
 CC schistosoma. The method may be used to treat fibrosis in a variety of
 CC tissues, particularly liver tissue, but also skin epidermis, skin
 CC endodermis, muscle, tendon, cartilage, cardiac tissue, pancreatic
 CC tissue, lung tissue, uterine tissue, neural tissue, pancreas,
 CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut
 CC tissue. The present sequence represents human IL-13bc.
 XX
 SQ Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 22; Length 380;
 Best Local Similarity 100.0%; Pred. No. 6.2e-198;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLATGCLYTLFISTFGCTSSDPEIKVNPQDFEIVDPGVLGYLYLQWQPPLSLD 60
 DB 1 mafvclaigclytlfistfgctssdteikvnpqdfelvdpgylgylylqwgppslsld 60
 QY 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLNKGIKTEAKHTLLPWQCTNGSEVQ 120
 DB 61 hfkectveyelkyrnigsetwktitknhykdgfdlnkgeakhtllpwqctngsevg 120
 QY 121 SSWAETTYWISPGIPETPKVQDMDCVYNNWOYLCSWKPGIGVLDTNLYNFYWEGLDH 180
 DB 121 sswaettywispggipetkvdqmdcvynwqyllycswkpgigvlltdnynlfywegldh 180
 QY 181 ALQCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFQOLNIVKPLP 240
 DB 181 alqcvdyikadgqngicrfpyleasdykdfyicvngssenkprrssytfqlqnvkplp 240
 QY 241 PVYLTFRESSCEIKLWSIPLGPIPARCFDYEIEIRDDDTLVATVENETYTLKTNE 300
 DB 241 pvyiltfressceiklwsiplgpiparcfdyeyeierrddtlvtatvenetytlktne 300
 QY 301 TRQICFVVRSKVNIYCSDDGIWSEMSDKQWEGEDLSKKTLLRFLWLPFGFILILVIFVTG 360
 DB 301 trqicfvvrskvniycsddgiwsewskqwedlskktllrflwlpfgfillilvifvtg 360
 QY 361 LLRKPNTPYKMWIPEFFCDT 380
 DB 361 llrkpntypkmipecfcdt 380

RESULT 10
 AAW36614
 ID AAW36614 standard; Protein; 380 AA.
 XX
 AC AAW36614;

XX 30-MAR-1998 (first entry)
 XX DT
 XX DE Human Zcytor2 cytokine receptor protein.
 XX KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 XX KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
 XX OS Homo sapiens.
 XX PN WO9733913-A1.
 XX PD 18-SEP-1997.
 XX PF 12-MAR-1997; 97WO-US04043.
 XX PR 13-MAR-1996; 96US-0013345.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
 XX PI O'Hara PJ;
 XX DR WPI; 1997-470820/43.
 XX DR N-PSDB; AAT96783.
 XX PS New nucleic acid encoding testis-specific cytokine receptor - useful
 XX PT for identification of ligands or antagonists, potentially for use as
 XX PT male contraceptives or for infertility treatment
 XX
 XX PS Claim 1; Page 51-53; 79pp; English.
 XX
 XX CC This sequence represents a novel ligand-binding receptor, Zcytor2, which
 XX CC shares homology with cytokine receptors and was isolated from a human
 XX CC testis cDNA library. The resulting polypeptide is a receptor for
 XX CC cytokines (particularly interleukin-13) and is expressed on the surface
 XX CC of testicular cells, probably being involved in spermatogenesis. It can
 XX CC be used to detect ligands that promote proliferation and/or
 XX CC differentiation of such cells in cultures and may also be used to treat
 XX CC infertility. Antagonists of this receptor may be used to characterise
 XX CC ligand-receptor interactions and as male-specific contraceptives. By
 XX CC blocking the action of IL-13, receptor antagonists and ligand-binding
 XX CC this receptor can also be used to modulate immune function, e.g. in
 XX CC allergy and asthma, as a diagnostic to determine circulating levels of
 XX CC ligand and also to isolate and purify ligands. Antibodies can be used to
 XX CC assay circulating receptor (an abnormal level may be indicative of
 XX CC disease such as cancer), for labelling cells that express the receptor,
 XX CC and therapeutically as antagonist.
 XX
 XX SQ Sequence 380 AA;

Query Match 98.8%; Score 2078; DB 18; Length 380;
 Best Local Similarity 99.2%; Pred. No. 2.2e-195;
 Matches 377; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFTTFCGTSSTDEIKVNPDPQFEIVDPGLVGLVQLWQPPPLSLD 60
 Db |||||
 QY 1 mafvclaigclyltfttfgtssstdeikvnpdpqfeivdpqylgylqlwqppplsl 60
 Db |||||
 QY 61 HFKECTVEYELKYRNIGSETWTKTITIKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
 Db |||||
 QY 61 hfkeytveyelkyrnisetwktitknlykdgfdlنگkieakihltlpwqctngsevg 120
 QY 121 SSWAETTYTSPQIGIPETKVDMDCVYNNQWYLCSKPKGIGVLLDTNYNLFWYEGLDH 180
 Db |||||
 QY 121 sswaettytspgipetkvgdmcdvynnwqylcswkpgigvlltdtnynlfwyegldl 180
 QY 181 ALQCVDYIKADGQNGICRFRFPLEASDYKDFYICVNGSSSENKPIRSSYFTFQLQNVKPLP 240
 Db |||||
 QY 181 alqcvdyikadgqngicrfrfpleasdykdfyicvngsssenkpirssyftfqlqnvkplp 240
 QY 241 PVYLTFRESSCEIKLKWISPLGPIPARCFDYEIEIREDDTTLVATVENETYTLTKTNE 300

Db |||||
 QY 241 pvyltfressceiklkwipglpiparcfdyeieireddttlvtatvenetytlktne 300
 QY 301 TRQLCFVVRSKVNIYCSDDGIWSEWSKQWEGEDLSKKTLLRFLWLPFGFILLIVIFVTG 360
 Db |||||
 QY 301 trqlcfvvrskvnlycsddgiwsewsdkqwegedskkllrfwlpfgfllilvifvtg 360
 QY 361 LLLRKPNTYPKMIEFFCDT 380
 Db |||||
 QY 361 llrkpntypkmieffcdt 380
 RESULT 11
 AAW36616
 ID AAW36616 standard; Protein; 372 AA.
 XX AAW36616;
 AC
 XX 30-MAR-1998 (first entry)
 DT
 XX Celebus macaque Zcytor2 protein.
 DE
 XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
 KW infertility; antagonist; contraceptive; diagnostic; therapeutic.
 XX KW
 XX Macaque sp.
 OS
 XX Key Location/Qualifiers
 FH Protein 1..372
 FT /label= Zcytor2
 FT /note= "partial protein sequence"
 XX
 XX WO9733913-A1.
 XX 18-SEP-1997.
 XX 12-MAR-1997; 97WO-US04043.
 XX 13-MAR-1996; 96US-0013345.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
 XX O'Hara PJ;
 XX WPI; 1997-470820/43.
 XX N-PSDB; AAT96784.
 XX
 XX New nucleic acid encoding testis-specific cytokine receptor - useful
 XX for identification of ligands or antagonists, potentially for use as
 XX male contraceptives or for infertility treatment
 XX
 XX Example 4; Page 56-57; 79pp; English.
 XX
 XX CC This sequence represents a novel ligand-binding receptor, Zcytor2,
 XX CC which shares homology with cytokine receptors and is isolated from
 XX CC testis tissue obtained from a Celebus macaque. The resulting polypeptide
 XX CC is a receptor for cytokines (particularly interleukin-13) and is
 XX CC expressed on the surface of testicular cells, probably being involved in
 XX CC spermatogenesis. It can be used to detect ligands promoting proliferation
 XX CC and/or differentiation of such cells in cultures and may also be used to
 XX CC treat infertility. Antagonists of this receptor may be used to
 XX CC characterise ligand-receptor interactions and as male-specific
 XX CC contraceptives. By blocking the action of IL-13, receptor antagonists and
 XX CC ligand-binding this receptor can also be used to modulate immune
 XX CC function, e.g. in allergy and asthma, as a diagnostic to determine
 XX CC circulating levels of ligand and also to isolate and purify ligands.
 XX CC Antibodies can be used to assay circulating receptor (an abnormal level
 XX CC may be indicative of disease such as cancer), for labelling cells that
 XX CC express the receptor, and therapeutically as antagonist.
 XX
 XX SQ Sequence 372 AA;

```
Query Match      88.1%; Score 1853; DB 18; Length 372;
Best Local Similarity 92.2%; Pred. No. 2.4e-173;
Matches 343; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 MAFVCLAGCLYFLISTTGTCTSSDTEIKVNPQDFEIVDPGGLYLYLQWQPPLSLD 60
DB 1 mafvylairclctflsttfgtstsdteikvnpqdfvdpqglvlylqwpplsl 60

QY 61 HFKECTVEYELKYNIGSEWTKTITNKLHYKDGFDLNGKEAKIHTLLPWOCNGSEVQ 120
DB 61 nfkectveyelkynigsetwtitnklhykdgfdlnkgleakihtllpwqctngsevg 120

QY 121 SSWAETTYWISPOGIPETKVDMDCVYNNWQYLLCSWKPGLVLLDTNLYNLFYWEGLDH 180
DB 121 sswaeatywispqgipetkvdmdcvynwqyllcswkpglvglltdnynlfwyegldr 180

QY 181 ALQCVDIKADQNGNIGRFRFYLEASDYKDFYICVNGSENKPIRSSYFTFQLOQIVKPLP 240
DB 181 alqcvdyikdgngnigrfylessdykdfyicvngssetkpirssyftfqlqnvkplp 240

QY 241 PVLTFTRSSCEITKLKWSIPLGPIPARCFDYETEIREDDTTLVTATVENETYTKTTNE 300
DB 241 pvlctctqeslyeiklkwslpplgpiparcfvyeireddttlvtatvenetyctikntne 300

QY 301 TRQLCFVVRKVNICYSDGDIWSEWSDKQCEWGEDLSKKTLLRFLWLPFGFTLLILVIEVTG 360
DB 301 trqlcfvvrskvnicysdgdiwsewskqceveeellkktllflpfgfillilvifvtg 360

QY 361 LLLRKNPTYPKM 372
DB 361 lllckrdsypkm 372

RESULT 12
AAW56261
ID AAW56261 standard; Protein; 315 AA.
XX AC AAW56261;
XX DT 16-SEP-1998 (first entry)
XX DE Mature interleukin-13 binding protein.
XX KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
XX KW autoimmune disease; antibody; immunotherapy.
XX OS Homo sapiens.
XX PN WO9810638-A1.
XX PD 19-MAR-1998.
XX PF 10-SEP-1997; 97WO-AU00591.
XX PR 27-FEB-1997; 97AU-0005374.
XX PR 10-SEP-1996; 96AU-0002262.
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;
XX DR WPI; 1998-207062/18.
XX DR N-PSDB; AAV22702.
XX PT New isolated interleukin-13 binding protein - used to develop
XX PT products for therapy e.g. for allergic conditions such as asthma or
XX PT for diagnosis or detection
XX PS Disclosure; Page 55-56; 69pp; English.
XX CC The IL-13 binding protein and related therapeutic molecules can be used
XX CC in the antagonism of at least one IL-13 activity. They can be used for
CC
```

CC treating IL-13 mediated conditions such as certain allergic conditions
CC such as asthma or to inactivate locally administered IL-13 after IL-13
CC treatment. The products can also be used as diagnostic agents, e.g. for
CC detecting autoimmune diseases. The antibodies can also be used for
CC immunotherapy and may also be used as a diagnostic tool.

XX Sequence 315 AA;

Query Match 83.3%; Score 1753; DB 19; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.2e-163;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 EIKVNPQDFEIVDPGGLYLYLQWQPPLSLDHFKECTVEYELKYNIGSETWTKTITKN 88
DB 1 eikvnpqdfvdpqglvlylqwpplsl dhfkectveyelkynigsetwtkitkn 60

QY 89 LHYKDGFDLNGKEAKIHTLLPWOCNGSEVQSSWAETTYWISPOGIPETKVDMDCVY 148
DB 61 lhykdgfdlnkgleakihtllpwqctngsevgsswaettywispqgipetkvdmdcvy 120

QY 149 NWQYLLCSWKPGLVLLDTNLYNLFYWEGLDHALQCVDIKADQNGNIGRFRFYLEASDYK 208
DB 121 nwqyllcswkpglvglltdnynlfwyegldhalqcvdyikadqngnigrcrfyleasdyk 180

QY 209 DFYICVNGSENKPIRSSYFTFQLOQIVKPLPPVYLTFTRESSCEIKLWSPILGPIPAR 268
DB 181 dfyicvngsenkpirssyftfqlqnvkplppvyltftressceiklkwslpkipar 240

QY 269 CFDEYEIREDDTTLVTATVENETYTKTTNETRQLCFVVRKVNICYSDGDIWSEWSDK 328
DB 241 cfdeyeireddttlvtatvenetytkttnetrqlcfvvrskvnicycsddgiwsewsk 300

QY 329 QCWEGEDLSKKTLLR 343
DB 301 qcwgedlskktllr 315

RESULT 13

AAW56260
ID AAW56260 standard; Protein; 359 AA.

XX AC AAW56260;

XX DT 16-SEP-1998 (first entry)

XX DE Construct containing mature interleukin-13 binding protein.

XX KW Therapeutic; IL-3 mediated condition; allergy; asthma; diagnosis;
XX KW autoimmune disease; antibody; immunotherapy.

XX OS Homo sapiens.

XX PN WO9810638-A1.

XX PD 19-MAR-1998.

XX PF 10-SEP-1997; 97WO-AU00591.

XX PR 27-FEB-1997; 97AU-0005374.

XX PR 10-SEP-1996; 96AU-0002262.

XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX PI Hilton DJ, Nicola NA, Simpson RJ, Zhang J;

XX DR WPI; 1998-207062/18.

XX DR N-PSDB; AAV22701.

XX PT New isolated interleukin-13 binding protein - used to develop
XX PT products for therapy e.g. for allergic conditions such as asthma or
XX PT for diagnosis or detection

PS Example 14; Page 52-53; 69pp; English.

XX The IL-13 binding protein and related therapeutic molecules can be used
 CC in the antagonism of at least one IL-13 activity. They can be used for
 CC treating IL-13 mediated conditions such as certain allergic conditions
 CC such as asthma or to inactivate locally administered IL-13 after IL-13
 CC treatment. The products can also be used as diagnostic agents, e.g. for
 CC detecting autoimmune diseases. The antibodies can also be used for
 CC immunotherapy and may also be used as a diagnostic tool.

XX Sequence 359 AA;

Query Match 83.3%; Score 1753; DB 19; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.5e-163;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 EIKVNPQDFEIVDPGLYGLYLQWQPLSLDHPFKECTVEYELKYRNIGSETWKTITITKN 88
 Db 45 eikvnpqdfeidvgylgylqlwqpplslidhfkectveyelkyrnigsetwktitkn 104

Qy 89 LHYKDGFDLNGKTEAKTHLLPWQCTNGSEVQSSWAETTTWISPGIPETKVDMDCVYY 148
 Db 105 lhykdgfdlnkgleakhtllpwqctngsevgsswaettywispqgipetkvqmdcvyy 164

Qy 149 NWQYLLCSWPKGIGVLLDTNLYNFWYEGDLHALQCVDYIKADGONIGCRFPYLEASDYK 208
 Db 165 nwqyllcswkpigvlldtnlynyfwyegdlhalqcvdylkadgqnlgcrfpyleasyk 224

Qy 209 DFYICVNGSSNKPIRSYFTFQONIVKPLPPVYLLFTRESSCEIKLWSIPLGPIPAR 268
 Db 225 dfyicvngssnkpirsyftfqonivkplppvylftressceiklwsiplgpipar 284

Qy 269 CFDEYIEIRDDTLVATVENETYLKTNETPQLCFVVRKSNVNIYCSDDGIWSEWSDK 328
 Db 285 cfdeyieirddtlvatvenetylkttnetpqlcfvvrksnvniycsddgiwsewsdk 344

Qy 329 QCWEGEDLSKKTLLR 343
 Db 345 qcwgedlskktllr 359

RESULT 14
 AAW35294
 ID AAW35294 standard; Protein; 383 AA.
 XX AAW35294;
 AC AAW35294;

XX 27-MAR-1998 (first entry)
 DT Murine IL-13 binding chain of the IL-13 receptor.
 XX

XX Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
 KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
 KW allergy; asthma; immune complex disorder.
 XX

OS Mus sp.
 XX

PH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= signal_sequence
 FT /note= "putative"
 FT 22..383
 FT Protein /label= mature_protein
 FT 22..334
 FT /label= extracellular_domain
 FT 335..356
 FT Domain /label= transmembrane_domain
 FT 357..383
 FT /label= intracellular_domain
 XX

W09731946-A1.

PD 04-SEP-1997.
 XX

XX 28-FEB-1997; 97WO-0503124.
 XX

XX 01-MAR-1996; 96US-0609572.
 XX

PA (GEMY) GENETICS INST INC.
 XX

XX Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
 PI Wood C;
 PI

XX WPI; 1997-448632/41.
 DR N-PSDB; AAT75213.
 DR

XX New nucleic acid encoding interleukin-13 receptor binding chain and
 PT transformed cells - proteins, antibodies and inhibitors, for
 PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
 PT and in diagnosis
 PT

XX Claim 11; Pages 30-31; 49pp; English.
 PS

XX The present sequence represents the murine interleukin-13 (IL-13) binding
 CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
 CC mediator of the known biological activities of IL-13. Recombinant
 CC IL-13bc proteins, and antibodies raised against them, are used to
 CC inhibit the binding of IL-13 to its receptor. They are particularly used
 CC to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex
 CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
 CC They are also used to treat immune deficiency (particularly in
 CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
 CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
 CC with such activity is combined with IL-13bc and the mixture applied.
 CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
 CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
 CC expression of IL-13, its receptor or binding chain, and to raise specific
 CC antibodies which may be useful for treating some tumours.
 XX

SQ Sequence 383 AA;

Query Match 56.8%; Score 1194.5; DB 18; Length 383;
 Best Local Similarity 58.9%; Pred. No. 9.1e-109;
 Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

Qy 1 MAFVCLAIGLTYFLJSTFTGCTSSSDTEIKVNPDPDFEIVDPGLYGLYLQWQPLSLD 60
 Db 1 mafv--hircicfillctitgys----leikvnpdpqdfeidvgylgylqwkppvvie 54

Qy 61 HFRECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNGKTEAKTHLLPWQCTNGSEVQ 120
 Db 55 kfkgtcleyelkyrnvdswkktittrnliykdgfdlنگkiegkirtlhsehctngsevg 114

Qy 121 SSAETTYWISPGIPETKVDMDCVYYNWQYLLCSWPKGIGVLLDTNLYNFWYEGDLH 180
 Db 115 spweasygisdegsetkiqdmkciyynwqylvcswkpgktyvsdntnytmffwyegldh 174

Qy 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSNKPIRSYFTFQONIVKPLP 240
 Db 175 alqcadylqhdnkvngcklnldssdykdficvngsskklpirssyvtvqlgnkvkplp 234

Qy 241 PVYLTFTRESSCEIKLWSIPLGPIPARCFDYIEIREDDTLVATVENETYLKTN 300
 Db 235 pefihisvensidirmkswstpggpiiprcytyelvireddiswesatdkndmklkrane 294

Qy 301 TROLCFVVRKSNVNIYCSDDGIWSEWSDKQWEGEDLSKKTLLRFLWLPFGFILLILVIFVTG 360
 Db 295 sedlcffvrckvnlvcaddgiwsewseececwgytgdpskxii-fivpvcffiflilllc 353

Qy 361 LLRLKPNTPYKPM 372
 Db 354 livekeepeptl 365

RESULT 15

AAV95295
 ID AAV95295 standard; Protein; 383 AA.
 AC AAV95295;
 XX 12-SEP-2000 (first entry)
 XX IL-13 binding chain of mouse IL-13 receptor.
 DE Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
 XX cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
 KW immune complex disease; lupus; nephritis; thyroiditis;
 KW Grave's disease; inflammatory; infection; therapy; antiallergic;
 KW antiinflammatory; antiasthmatic; vaccine.
 XX Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "signal peptide"
 FT Protein 22..383
 FT /note= "mature protein"
 FT Domain 22..334
 FT /note= "extracellular domain; a polypeptide
 FT comprising amino acids 22-334 is
 FT specifically claimed in Claim 11(b)"
 FT Domain 335..356
 FT /note= "transmembrane domain"
 FT Domain 357..383
 FT /note= "intracellular domain; a polypeptide
 FT comprising amino acids 257-383 is
 FT specifically claimed in Claim 11(c)"
 XX
 PN WO200036103-A1.
 XX 22-JUN-2000.
 XX 13-DEC-1999; 99WO-US29493.
 XX 14-DEC-1998; 98US-0211335.
 XX (GEMY) GENETICS INST INC.
 XX (UWJO) UNIV JOHNS HOPKINS.
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 FI Wills-Karp M;
 XX WPI; 2000-431587/37.
 XX N-PSDB; AAA27911.
 XX
 PT New polynucleotide encoding an interleukin-13 (IL-13) binding chain of
 PT an IL-13 receptor for treating IgE-mediated conditions, such as atopy,
 PT asthma, Grave's disease and inflammatory conditions of the lung -
 XX Claim 11(a); Page 50-51; 60pp; English.
 XX
 CC The present sequence is that of the interleukin-13-binding chain
 CC (IL-13bc) of the murine IL-13 receptor, as deduced from an isolated
 CC C3H/HeJ mouse thymus cDNA clone (see AAA27911). IL-13bc is a member
 CC of the haematopoietin receptor family that acts as a mediator of
 CC IL-13. The invention provides methods for the recombinant
 CC production of IL-13bc polypeptides, including claimed full-length
 CC IL-13bc, its extracellular domain, and its intracellular domain.
 CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,
 CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction
 CC of IL-13 and its receptor) can be used to treat conditions in
 CC which IL-13 is implicated, particularly IgE-mediated conditions and
 CC diseases including atopy, allergy, asthma, immune complex diseases
 CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,
 CC thyroiditis and Grave's disease), lung inflammation,
 CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage
 CC activation, IL-13bc proteins can also be used to enhance macrophage

CC activation, e.g. in vaccination, treatment of mycobacterial or
 CC intracellular organisms or parasite infections. IL-13bc proteins
 CC may also be used to potentiate the effects of IL-13 in vitro and
 CC in vivo, as diagnostic agents, and to screen for agents capable of
 CC binding to IL-13bc or IL-13 receptor, or which interfere with the
 CC binding of IL-13 to its receptor.
 XX
 SQ Sequence 383 AA;

Query Match 56.88; Score 1194.5; DB 21; Length 383;
 Best Local Similarity 58.9%; Pred. No. 9.1e-109;
 Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
 QY 1 MAFVCLALGCLYTFELISTFTGCTSSDTEIKVNPQDFEIVDPCYLGVLQWPPSLD 60
 DB 1 mafv--hircfcilictitgys---leaknpqdfelidpallgylqlwppvvie 54
 QY 61 HFRECTVEYELKYRNIGSETWTKTITIKNLHYKDGFDLKNKIEAKIHTLLPMQCTNGSEVQ 120
 DB 55 kfgctleyelkyrnvdsgsktitiitnlykdgfdlnkgiegkirthlsehtngsevg 114
 QY 121 SSWAETTYWISPOGIPETKVDMDCVYNNQYLLCSKPKGIGVLLDTNLYNLFYVEGLDH 180
 DB 115 spwieasygisdegslctkiqdmkciyynwqylvcskpgktytsdntymffwyegldh 174
 QY 181 ALQCVDYIKADGQNGICRFPYVLEASDYKDFYICVNGSSENKPIRSSYFTFOLQNVKPLP 240
 DB 175 alqcadyiqhdekngvcklnldssdykdficvngsskpieprrssyvtvqlqlnvkplp 234
 QY 241 PVYLTFTRESSCEIKLWSIPLGPAPARCFDYEIEIREDDTTLVATVENEYTLTKTTNE 300
 DB 235 pefihisvensidirmkwtstpggpiprcyeyeiaveddiswesatdkndmkkrane 294
 QY 301 TRQICFVVRKVNIIYCSDDGIWSEWSKQCEWGEDLSKKTLLRFLWLPFGFILLIVFTVG 360
 DB 295 sedicffvrckvniycaddgiwsewseecewgytgpdkkii-fivpvcilffillilc 353
 QY 361 LLRRKPNTYPKM 372
 DB 354 livekeepeptci 365

Search completed: September 1, 2001, 19:07:03
 Job time: 70 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:05:53 ; Search time 43.66 Seconds
(without alignments)
662.994 Million cell updates/sec

Title: US-09-077-817-2

Perfect score: -2104

Sequence: 1 MAFVCLAIGCLYFLISTTF.....LLLRPNTPYKMPIEFFCDT 380

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	311.5	14.8	420	2 S21052	interleukin-5 rece
2	292	13.9	335	2 A40267	interleukin-5 rece
3	263	12.5	831	2 J01655	prolactin receptor
4	247	11.7	415	2 S12357	interleukin-5 rece
5	220	10.5	369	2 A42565	interleukin-2 rece
6	216.5	10.3	830	2 I50455	prolactin receptor
7	212.5	10.1	369	2 I49280	interleukin-2 rece
8	208	9.9	373	2 A55718	interleukin-2 rece
9	195	9.3	878	1 A40091	interleukin-3 rece
10	180.5	8.6	897	1 A39255	cytokine receptor
11	178	8.5	896	2 I56563	interleukin-3 rece
12	173.5	8.2	896	1 A35782	cytokine receptor
13	165	7.8	310	2 A29884	prolactin receptor
14	165	7.8	412	2 A41070	prolactin receptor
15	165	7.8	581	2 I45971	prolactin receptor
16	165	7.8	610	2 A34631	lactogen receptor
17	165	7.8	610	2 A36116	prolactin receptor
18	160.5	7.6	303	2 I77524	prolactin receptor
19	159	7.6	292	2 I77525	prolactin receptor
20	159	7.6	608	2 I53269	prolactin receptor
21	151	7.2	622	2 A40144	prolactin receptor
22	150.5	7.2	917	2 I49699	glycoprotein 130 -
23	149	7.1	616	2 A30304	prolactin receptor
24	142.5	6.8	400	2 S06945	granulocyte-macrop
25	138	6.6	378	2 A40266	interleukin-3 rece
26	134.5	6.4	1097	2 S17368	leukemia inhibitor
27	133.5	6.3	333	2 S13684	granulocyte-macrop
28	133.5	6.3	378	2 S50040	granulocyte-macrop
29	131.5	6.2	630	2 I51086	prolactin receptor

ALIGNMENTS

RESULT 1

S21052

interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S21052; S21053; A46175; S78106; S78107
R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A;Title: Molecular cloning and expression of the human interleukin 5 receptor.
A;Reference number: S21050; MUID:92121815
A;Accession: S21052
A;Molecule type: DNA
A;Residues: 1-420 <MUR>
A;Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A;Experimental source: clone lambda h5R.12
A;Accession: S21050
A;Molecule type: DNA
A;Residues: 1-395, 'I' <MU2>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A;Experimental source: clone lambda h5R.27
A;Accession: S21053

30	129	6.1	150	2	B34631	lactogen receptor
31	126.5	6.0	918	2	A36337	membrane glycoprot
32	122.5	5.8	286	2	S50039	granulocyte-macrop
33	120.5	5.7	771	2	B38252	granulocyte colony
34	120.5	5.7	783	2	JH0329	granulocyte colony
35	120.5	5.7	863	2	C38252	granulocyte colony
36	112.5	5.3	1630	2	C41214	protein-tyrosine-p
37	111.5	5.3	1557	2	D41214	titin - tyrosine-p
38	110	5.2	6805	2	S20901	titin - rabbit (fr
39	109.5	5.2	918	2	A44257	interleukin-6 sign
40	109.5	5.2	26926	1	I38344	titin, cardiac mus
41	107.5	5.1	638	2	A33991	somatotropin recep
42	107.5	5.1	837	2	A34898	granulocyte colony
43	106	5.0	634	2	S33339	somatotropin recep
44	105.5	5.0	1825	2	T32828	hypothetical prote
45	104.5	5.0	1092	2	JX0312	differentiation-st

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 333-420 <TAV>
A;Experimental source: HL-60 cells and eosinophils
A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R;Murata, Y.
submitted to the EMBL Data Library, July 1991
A;Reference number: S78106
A;Accession: S78106
A;Molecule type: DNA
A;Residues: 1-128, 'I', 130-395, 'I' <MUW>
A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
R;Murata, Y.
submitted to the EMBL Data Library, September 1991
A;Reference number: S78107
A;Accession: S78107
A;Molecule type: mRNA
A;Residues: 1-128, 'I', 130-332, 'K' <MU4>
A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>

F:345-365/Domain: transmembrane #status predicted <TM>
F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.8%; Score 311.5; DB 2; Length 420;
Best Local Similarity 26.9%; Pred. No. 3.1e-17;
Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPQDFEIVDGYLYLQWOPPLSLDHFKECTVEYELKYNIGSETWKTIIT 86
DB 25 DEKISLLPVNFTIKVTG-LAQVLLQWKPDPQEQ-RNVNLEYQVKINAPKEDDIYETRI 82
QY 87 KNLHYKDGFLNKGIEAKIHTLLPQCTNGSEVSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES---KCVTILHKGFSASVRILO---NDHSILLASSWASAEHL-APGSPGTSVNLCT 135
QY 147 -----YNNQYLL-CSWKGIGVLLDTNLYFY----WYEGDLHALQCVDIKAD 191
DB 136 TTTTNDYNSRLRSYQVSLHCTWLVGTDAPEDTQFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLNIVKPLPPVYLFT 248
DB 190 LGRNIACWFPRTFILSKGRDMLVNGSSSAIRPFDQLFALHAIQINPLNVTAEI 249
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVATVENETTYLTKTNETRQLCFV 308
DB 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIHNRNGYLQIEKLMTNFAISIIDDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSESDKOCWGEDLSKTLIRFWMPLPGFIIL-----VIFVGLL 362
DB 309 RAAVSSMCREAGLWSEWS-QPIYGVNDEHKP--LREW---FVIVIMATICFILLLSLI 361
QY 363 LRKPNTYPMKP 374
DB 362 KCICHLWIKLFP 373

RESULT 2
A40267
Interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tuijens, T.; Van der Heyden, J.; Fiers, W.; Pl
Cell 66, 1175-1184, 1991
A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-spec
A:Reference number: A40267; MUID:92005669
A:Accession: A40267
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <TAV>
A:Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
C:Keywords: cytokine receptor; transmembrane protein

Query Match 13.9%; Score 292; DB 2; Length 335;
Best Local Similarity 28.0%; Pred. No. 8.2e-16;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

QY 27 DTEIKVNPQDFEIVDGYLYLQWOPPLSLDHFKECTVEYELKYNIGSETWKTIIT 86
DB 25 DEKISLLPVNFTIKVTG-LAQVLLQWKPDPQEQ-RNVNLEYQVKINAPKEDDIYETRI 82
QY 87 KNLHYKDGFLNKGIEAKIHTLLPQCTNGSEVSSWAETTYWISPOGIPETKVQDMDCV 146
DB 83 ES---KCVTILHKGFSASVRILO---NDHSILLASSWASAEHL-APGSPGTSVNLCT 135
QY 147 -----YNNQYLL-CSWKGIGVLLDTNLYFY----WYEGDLHALQCVDIKAD 191
DB 136 TTTTNDYNSRLRSYQVSLHCTWLVGTDAPEDTQFLYRYGSWTE-----ECQEYSKDT 189
QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLNIVKPLPPVYLFT 248
DB 190 LGRNIACWFPRTFILSKGRDMLVNGSSSAIRPFDQLFALHAIQINPLNVTAEI 249

DB 190 LGRNIACWFPRTFILSKGRDMLVNGSSSAIRPFDQLFALHAIQINPLNVTAEI 249
QY 249 ESSCEIKLWSIPGLPIPARCFDYEIREDDTTLVATVENETTYLTKTNETRQLCFV 308
DB 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIHNRNGYLQIEKLMTNFAISIIDDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSEWS 326
DB 309 RAAVSSMCREAGLWSEWS 326

RESULT 3

JQ1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
A:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: JQ1655; MUID:93075121
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A:Experimental source: kidney
A:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 12.5%; Score 263; DB 2; Length 831;
Best Local Similarity 26.4%; Pred. No. 5.3e-13;
Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

QY 18 TTGCTSSSTETKVN---PPQDFE---IVDPG-----YLYLYLQWOPPLSL 59
DB 97 TTFNTITVATNEIGSSSDPQYVDVTSIVQSPVNLTLTKRSANTMYLWAKWSPPLA 156
QY 60 DHFKECTVEYELKYNIGSETWKTIITKNLHYKDGFLNKGIEAKIHTLLPQCTNGSEV 119
DB 157 DASSNHLHYELRLKPEKEWEETI---SVGVQTOCKINR-LNAGMYVYVQVRCITLDPGE 212
QY 120 QSSWAETTYWISPOG-IPETKVQDMDCVYNNQYLLCSWKGIGVLLDTNLYFYWYEG 178
DB 213 WSEWSSERHILPSGQSPPEKPTTIKCRSPEKETFTCWKPKGLDGGHTNVTLLYSKEGE 272
QY 179 DHALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQQLNIVK 238
DB 273 EQVECPDY-RTAGPN-SCYFDKKHTSFWTYINITVATNEIGSSSDPQYVDVTSIVQ 330
QY 239 LPVVLFTTRESSCEIK---LKWS-IPGLPIPARCFDYEIETIR---EDDTTLVATVEN 290
DB 331 DPPVNVLELKKPINRKPDLVLTWSPPLADVRSGWLTLEYELKPEEGEWEETIFVQ 390
QY 291 ET-YTLKTTNETRQLCFVVRSKVNIYCSDD--GIWSEWSDKQWE-GEDLSKTLIRFWL 346
DB 391 QTOYKMFSLNPGKYI-----IQIHCCKPDHGSWSESENVIQIPNDFRVKDMI-VWI 443
QY 347 PFGFI--LILVIFVTGLLRLKPNTPYKMP 374
DB 444 VLGVLSLICLIMSWTMYLKYRMITMLP 473

RESULT 4

SL2357
Interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)

R;Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.
Hum. Mol. Genet. 2, 1099-1104, 1993
A:title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-lll
A:Reference number: I54332; MUID:94004847
A:Accession: I54332
A>Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:I.LI9546; NID:g349631; PIDN:AAC37524.1; PID:g349632
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1: IMD4
A:Cross-references: GDB:134807; OMIM:308380
A:Map position: Xq13.1-Qx13.1
A:Introns: 39/1; 50/2; 152/1; 198/3; 253/1; 285/2; 308/3
A>Note: defects are associated with an x-linked form of severe combined immunodeficiency
C:Superfamily: Interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunodeficiency

Query Match 10.5%; Score 220; DB 2; Length 369;
Best Local Similarity 25.5%; Pred. No. 4.9e+10;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

QY 97 LNKGIEAKIHITLIPWQTNGSE-VOSSWAETTWISQGIPETKVQMDDCVYNQVLLC 155
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 19 LGVGLNTIIIT-----PNGNEEDTADFTTTMTPTDSLVSSTLPPEVQCFFVNVEYMNC 72
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 156 SW-----KPGIGVLLDTNTNLFWBYEGLDH--ALQCVDYIKADQNIGCRFPYLEASDY 207
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 73 TWNSSSPQP-----TNLTWHYKNSDNCKVKOKSHLYFSEEITSGCQLKKKEIHLY 125
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 208 KDFYCIVGVSSSENKPRISSYFTFOLQNIAPPLPPVIYTFTRESSCEIKLWSPIPLGPIPA 267
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 126 QTFVVQLQDPRE--PRQAOTMLKLQNLVIPAPENLTHLKSQSLELNWN---NRFLN 180
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 268 RCFDYEIERE-DTTLVTATVE-NETYTKTNETRQLCFVVRSKVINCYDDGIINSEW 325
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 181 HCLEHLVQYRTDWDSHWTEQSDVRYHRKFSLPSVDGQRKYTRFRSRENPLCGSAQHWESEW 240
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 326 SDKOCWGEDLSKTLLRFWLPGFIILLIFVYG 360
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 241 SHPIHW-GSNTSKEN-----PFLFAEVVISVG 268
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 6
I50455
prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor
A:Reference number: I50455; MUID:94283267
A:Accession: I50455
A>Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: EMBL:U07694; NID:g456381; PIDN:AAA20646.1; PID:g456382
C:Superfamily: cytokine receptor homology
F;36-220/Domain: cytokine receptor homology <CRSL>
F;240-426/Domain: cytokine receptor homology <CRS2>

Query Match 10.3%; Score 216.5; DB 2; Length 830;
Best Local Similarity 24.4%; Pred. No. 2.6e+09;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;

QY 18 TFGCTSSDSTEIKVPNPQQDFEIVDPGYLG-----YLYLOW 53
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 97 TTNTITVMANNEIGSNS-----DPOYDVTSIQDPAPNVLSLETHTTASTYYLLAKW 150
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 54 QPPLSLDHFEKTV-EYELKYRNIGSETWKTIITKNLRHYDGFDLNKGIEAKIHITLLPWQ 112

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151 SPPLADVTSNHYVYELRLKPEKEWETV---SVGQYQYKVNRLQAGVYVYQVR 206
QY 113 CTNSEVOSSWAETIYISPOG-IPETKQVDMDCVYVYVQYLLCSWPGICVGLDNTYNL 171
Db 207 CVLDIGENSESSERHIHIPNGESPPKPTIIKRSPEKETFTCWKPGSDGGHPTNYTL 266
QY 172 FWVEGLDHALQVDYIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQ 231
Db 267 LYSKEGERVECDPY-KTAGPN-SCYFDKKHTSFWIYNTVATNEIGSNVSDPLYVD 324
QY 232 LONIVKPLPPVYLFTRESSCEIK----LKWS-IPLGPIPA--RCFDYIEIREDDTTLV 284
Db 325 VYIIVQDTPPVNVITLKKTKVNRKPYLVLTWSPPLADVRSGWLTLDYELRLKPEEA--- 381
QY 285 TATVENETIYLTNETRQICFV---RSKNVNYCSD--GINSWS-DKQCEGEDLS 337
Db 382 -----EWEETIFVQOOTHYKMFSLNPGKKYIVQIHCXPDHGHGSWSSELSKYLOIPTDFR 436
QY 338 KKTLLRFLWLPFGFILLIVFV 358
Db 437 IKDMV-VWIIVGLSSLICLV 456

RESULT 7
149280
interleukin-2 receptor gamma chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: I49280; JN0592; JN0775; S37582; I53398
R:Cao, X.; Kozak, C.A.; Liu, Y.
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) g
A:Reference number: A47514; MUID:93391374
A:Accession: I49280
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <CAO>
A:CROSS-references: EMBL:U21795; NID:g727349; PIDN:AAA64279.1; PID:g727350
A:Accession: A47514
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE2>
A:CROSS-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of func
A:Reference number: JN0592; MUID:93277575
A:Accession: JN0592
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KUM>
A:CROSS-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <KOB>
A:CROSS-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
R:Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
A:Reference number: S37582
A:Accession: S37582
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:CROSS-references: EMBL:X75337
R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal l

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A:Reference number: I53398; MUID:95104285
A:Accession: I53398
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:CROSS-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
C:Genetics:
A:Gene: IL-2Rgamma
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
A:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), bet
eptors.
C:Function:
A:Description: receptor for interleukin-2
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
F;256-284/Domain: transmembrane #status predicted <TM>
F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) #status predict
Query Match 10.1%; Score 212.5; DB 2; Length 369;
Best Local Similarity 26.9%; Pred. No. 1.9e-09;
Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;
QY 136 PETKVQDMDCVYVYVNOYLLCSW----KPGIGVLDNTNLYFWYEGLDHAL--OCVDYIK 189
Db 53 PTLPLPEVQCFVFNIEYMNCTWNSSEPPQA-----TNLTLYRYKVSNDNTFQCSHYLF 107
QY 190 ADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQIQNIYKPLPPVYLTRE 249
Db 108 SKEITSGCQIKEDIQLYQYFVVQL--QDPQKQRAVQKLNQLNVLPRAPENLTLSNL 165
QY 250 SSCBIKLKWSIPLGPIPARCFDYIEIREDD--DTTLVATVENE--TYILKTNETNRQICFV 307
Db 166 SESQLELRWK--SRHIKERCLQYLVQYRSNDRSMTIELIVNHPEFRLSPVDELKRYTFR 223
QY 308 VRSKNVNYCSDDGWSWSKQCEG-----EDLSKTKLLRFLWLPFGF--ILILVIFVYGL 361
Db 224 VRSRYNYICGSSQWQSKQSPVHWSHTVEINPSLFAELVILPVGTMLIITLIFVYCW 283
QY 362 LLRKPNTPY 370
Db 284 LERMPPIPP 292

RESULT 8
A5718
interleukin-2 receptor gamma chain precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
C:Accession: A5718
R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg
Genomics 23, 69-74, 1994
A:Title: IL-2gamma gene microdeletion demonstrates that canine X-linked severe combi
A:Reference number: A5718; MUID:95130114
A:Accession: A5718
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <HEN>
A:CROSS-references: GB:U04361; NID:g517411; PIDN:AAC48403.1; PID:g517412
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication
Query Match 9.9%; Score 208; DB 2; Length 373;
Best Local Similarity 26.0%; Pred. No. 4.5e-09;
Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;
QY 115 NGSE-----VQSSWAETIYISPOGIPETKYQVDMDCVYVYVNOYLLCSW-----KPGI 161
Db 31 NGNEDITPDPFLATPSET---LSVSLPLPEVQ---CFVFNVEYMNCTWNSSEPRP-- 82

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Db   358 YSLHWETQKIP--KYIDHTFVOYKKSSWKSDKTENLRVNSMDLPQLEPDTSYCAR 414
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy   308 VRSK-VNIYCDDGIWSEWSDKOCWEGEDLSKTKLLRFLWLPFGFILILVIVFTGLLL 363
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db   415 VRVKPISDY---DGINSENSNEYTWT-TDVMPTL---WI-----VLILVFLIFLTLL 460
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 10
A39255
Cytokine receptor common beta chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C;Accession: A39255
R;Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A;Title: Molecular cloning of a second subunit of the receptor for human granulocyte-
A;Reference number: A39255; MUID:91088571
A;Accession: A39255
A;Molecule type: mRNA
A;Residues: 1-897 <HAY>
A;Cross-references: GB:M38275
C;Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
C;Genetics:
A;Gene: GDB:CSF2RB
A;Cross-references: GDB:I126838; OMIM:138981
A;Map position: 22q13.1-22q13.1
C;Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C;Keywords: alternative splicing; cytokine receptor; duplication; transmembrane prote
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-897/Product: cytokine receptor common beta chain #status predicted <MAT>
F;17-443/Domain: extracellular #status predicted <EXT>
F;35-232/Domain: cytokine receptor homology <CRS1>
F;250-431/Domain: cytokine receptor homology <CRS2>
F;444-460/Domain: transmembrane #status predicted <TM>
F;461-897/Domain: intracellular #status predicted <INT>

Query Match          8.6%; Score 180.5; DB 1; Length 897;
Best Local Similarity 22.6%; Pred. No. 2.1e-06;
Matches 90; Conservative 58; Mismatches 146; Indels 105; Gaps 21;

Qy   32 VNPDPDFEIVDPGLGY-----LYLOWQP-----LSLDHF----- 62
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db   97 VIPQSFWITDVDFSPDRPLGTRUTVTLTQHVPPEPRDLQISTDQDHFLTWSVAL 156
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy   63 -----KECTVEYEIKRYNIGSETWK--TIITKNLHYKDGFNLKGIE-----A 103
      :||::||::||::||::||::||::||::||::||::||::||::|||
Db   157 GSPQSHWLSPCDLEFEVVYKRLL-QDSWEDAAILLSNTS-----QATLGPEHLMPSSYYVA 210
      :||::||::||::||::||::||::||::||::||::||::||::|||
Qy   104 KIHT-LLPWOCTNGSEVOSSWAETTYIISQGITPKVKQDMDCVYYNQWILLCSWKPGIG 162
      ::||::||::||::||::||::||::||::||::||::||::||::|||
Db   211 RVRTRLAPGSRLSGR--PSKSWPEVCWDSPQG-DEAQPNLECFCFDGAALVSCSWERYKE 267
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy   163 VLLDTNTNLFVYBGLDHALQCVDYIKADGNQIG-----CRFPYLEASDYKDFYICVN 215
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db   268 VASSVSFGLFKYKPSPDAGEECSPVLR---EGLSLTRHHHCQIPVPPDATHGYIVSVQ 324
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy   216 GSSENKPIRSYTFQLQNVKPLPPVYLTTRESSCEIKLKWSSIPGLPIPARCFDYEIE 275
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db   325 PRRAEKHIKSSV-----NI-QMAPPSLVNTKGDG-SYSLRWETMKWRVEHDHTTEIQ 375
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy   276 IREDDTLIVTAT-VENETYILKITTN-----ETQLCLFV-VRSKVNYICSDDGTWSE 324
      :||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db   376 YRKD-----TATWKDSKETETLQNAHSMALEPALESTPYWARVRVRTSGY---NGIWE 427
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy   325 WSKQOCWEGEDLSKTKLLRFLWLPFGFILILVIVFTGLLL 363
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db   428 WSEARSWDTSV-----LPMWVLIIVIFLTAVL 457
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 11
156563
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interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56563
R:Appel, K.; Butlini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and A:Reference number: I56563; MUID:95370942
A:Accession: I56563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
C:Genetics:
A:Gene: rIL-3Rbeta
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-433/Domain: cytokine receptor homology <CRS2>
F:23-441/Domain: extracellular #status predicted <EXT>
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-434/Domain: cytokine receptor homology <CRS2>
F:442-463/Domain: transmembrane #status predicted <TM>
F:464-896/Domain: intracellular #status predicted <INT>

Query Match 8.5%; Score 178; DB 2; Length 896;
Best Local Similarity 21.4%; Pred. No. 3.3e-06;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;
QY 5 CLAIGCL--YT-FLISTTFTGCTSSSDTEIKVN-----PPQDFEIVDPGILGYL 49
Db 94 CVPRRCVLPYTFQSVSKEDYISLPDRDLSHLVPLAQHVQPPPKDISPSG--DHF 151
QY 50 YLQWQPL---SLDHFKECTVEYELKYNIGSETWTKIITKNLHYKDGFDLNGKIEAKIH 106
Db 152 LLKWSVSLGDAQVSLLSQKQDFEYAYKQL--QDSWED--ASSLW-----TCNLWVTLEPK 203
QY 107 TLLP-----WQCTNGSEVQ---SSWAETTYWISPOGIPETKQVDMDCVYNNWQYLL 154
Db 204 LFLPNSIYAVRAQLAPGSLSGRSGWSPVHWDSPTE-DKARPQNLCQFFDGIOQLN 262
QY 155 CSWPGIGVLLDTNLYNFWYEGDLHALQCVDIKADGQNGICRFPFYLEASDYKDFYICV 214
Db 263 CSWEVWKVTDVSFGLFYSSPKAGEKCSVVKE-----LQASRYTRYHCSL 311
QY 215 NGSENPIRSSYTFQLO-----NIVKPLPP-VLFTTRESSCEIKLKWISPL 262
Db 312 NVSD---PAASHQYTSVSKRLEQKGFIESHIQMNPTLNLTKNRDS---YSLHWETQK 365
QY 263 GPIPARCFDYEIR-----EDDTTLVATVENETTLKTTNETRQLCFVRSKVNICY 316
Db 366 MSYPIQAHAFQVYKKLDRWDSKT-----ENLHAHSMDLPOLEPQTSYCARVRVTIP 421
QY 317 SDDGIWSEWSDKQCEGEDLSKTLRLFWLPFGFILILVIFVTGLLL 363
Db 422 EYKGLWSEWSECTWT-TDWMPTL---WI-----VLILVFLILTLFL 460

RESULT 12
A35782
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A35782
R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Aral, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protein
A:Reference number: A35782; MUID:90319131
A:Accession: A35782
A:Molecule type: mRNA
A:Residues: 1-896 <GOR>
A:Cross-references: GB:M34397; NID:g191821; PIDN:AAA37204.1; PID:g309101
C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 receptor
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-896/Product: cytokine receptor common beta chain #status predicted <MAT>

Query Match 8.2%; Score 173.5; DB 1; Length 896;
Best Local Similarity 20.7%; Pred. No. 7.5e-06;
Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;
QY 5 CLAIGCLYTFLLISTTFTGCTSSSDTEIK-----VNPQDFEIVDPGILGYL 48
Db 94 CVPRRCVLPY---TRFSITNEDYISFRPDSDLGIQLMPLAQNVQPPPLPKNVSSISSEDR 150
QY 49 LYLQWQPL---SLDHFKECTVEYELKYNIGSETWTKIITKN-----LHYKDGFDLNGK 100
Db 151 FLLEWSVSLGDAQVSWLSSKDIIEFVAYKRL-QDSWEDAYSHTSKFQVNPPEKFLPLNS 209
QY 101 IEA-KIHT-LLPWQCTNGSEVQSWAETTYWISPOGIPETKQVDMDCVYNNWQYLLCSWK 158
Db 210 IYAPRVTRLYPGSSLSGR--PSRWSPEAHWDSPG-DKAQPQNLCQFFDGIOQLSHCSWE 266
QY 159 PGIGVLLDTNLYNFWYEGDLHALQCVDIK-ADGQNI-----GCRFPYLEASDYKDFYIC 213
Db 267 VWTQTGTSVSFGLFYRPSVPVAPBEKCSVPVKEPGASVTRYHCSLPPPEPSAHSQYTVS 326
QY 214 VNGSENKPIRSSYTFQLOINIVKPLPPVLTFTRESSCEIKLKWISPLGIPARCFDYE 273
Db 327 V-----KHLEQKGFIMSYNHIQMEPTLNLTKNRDS---YSLHWETQKWAYSFIETFFQ 377
QY 274 IEIREDDTLVATVEN--ETYTLKTTNETRQLCFVRSKVNICYSDGIGWSEWSDKQCV 331
Db 378 VOYKKKSDSWEDSKTENLDRAHSMDLSQLPDTSYCARVRKVPISNVYDGIWSEWSEYTW 437
QY 332 EGEDLSKTLRLFWLPFGFILILVIFVTGLLL 363
Db 438 K-TDWMPTL---WI-----VLILVFLILTL 461

RESULT 13
A29884
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C:Accession: A29884
R:Boutin, J.M.; Jolicœur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banvi
Cell 53, 69-77, 1988
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth
A:Reference number: A29884; MUID:88165059
A:Accession: A29884
A:Molecule type: mRNA
A:Residues: 1-310 <BOU>
A:Cross-references: GB:M19304; NID:g206364; PIDN:AAA1937.1; PID:g206365
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-310/Product: prolactin receptor #status predicted <MAT>
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 7.8%; Score 165; DB 2; Length 310;
Best Local Similarity 28.5%; Pred. No. 9.2e-06;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;
QY 131 SPQIPETKQVDMDCVYNNWQYLLCSWKPGIGVLLDTNLYNFWYEGDLHALQCVDIKA 190
Db 21 SPQKPEIH----KCRSPDKETFTCWNNPCTDGLPTNYSILTSYKGEKTYECPDY-KT 75
QY 191 DQGNICRFPYLEASDYKDFYICVN-----GSSENKPIRSSYTFQLOINIVKPLPPVLT 245
Db 76 SGPN-SCFFSKQYTSIWKIIVITVNATNQMGSSSDPL-----YVDVTYIVEPEPPRNL 129

Search completed: September 1, 2001, 19:07:53
Job time: 120.sec

RESULT 15
I45971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol.Cell. Endocrinol. 89, 47-58, 1992
A:title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
A:Reference number: I45971; MUID:93246019
A:Accession: I45971
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:08 ; Search time 68.62 Seconds
(without alignments)
732.671 Million cell updates/sec

Title: US-09-077-817-2

Perfect score: 2104

Sequence: 1 MAFVCLAIGCLTFLISTTF.....LLLRKNTYKMIPEFCDT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1194.5	56.8	383	11	O88786
2	311.5	14.8	420	4	Q14633
3	310.5	14.8	396	4	Q14631
4	298.5	14.2	415	11	Q920K4
5	292	13.9	333	4	Q15469
6	264.5	12.6	349	6	Q97597
7	241.5	11.5	279	4	Q9UDY5
8	197.5	9.4	363	13	Q9DEQ1
9	187	8.9	611	13	Q9PTI0
10	187	8.9	611	13	Q9IBF6
11	178	8.5	896	11	Q64146
12	174.5	8.3	611	13	Q9PHH9
13	173.5	8.2	881	13	Q57519
14	170	8.1	890	11	Q921A0
15	167	7.9	622	6	Q9N077
16	165	7.8	296	6	O18880
17	164	7.8	227	6	Q9GLW3
18	159	7.6	581	6	O46561
19	156	7.4	625	6	Q9XS92

Q9W6U9 gallus gall
O46386 mustela vis
Q16354 homo sapien
Q9UHJ5 homo sapien
Q9DU00 sparus aura
Q9UHH5 homo sapien
O75462 homo sapien
Q9Jm58 mus musculu
Q9ueh7 homo sapien
Q93404 oreochromis
O48985 cervus elap
Q9uq41 homo sapien
Q9hc73 homo sapien
Q13594 homo sapien
Q13593 homo sapien
Q13592 homo sapien
Q9vwe0 drosophila
Q9myl1 macaca mula
Q9myk9 macaca mula
Q9myl2 macaca mula
Q9myl0 macaca mula
Q92919 homo sapien
Q92920 homo sapien
Q92921 homo sapien
Q9jkg1 cavia porce
Q28733 oryctolagus

ALIGNMENTS

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RESULT 1
O88786 ID O88786 PRELIMINARY; PRT; 383 AA.
AC O88786;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IL-13 RECEPTOR ALPHA 2.
GN IL13RA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ; TISSUE=THYMUS;
RX MEDLINE=98391042; PubMed=9725226;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,
RA Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,
RA Collins M.;
RT "The murine IL-13 receptor alpha 2: molecular cloning,
RT characterization, and comparison with murine IL-13 receptor alpha 1.";
RL J. Immunol. 161:2317-2324(1998).
DR EMBL; U65747; AAC33240.1; -.
DR MGI; MGI:1277954; IL13ra2.
DR InterPro; IPR002996; -.
DR InterPro; IPR003532; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN1.
SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;

Query Match 56.8%; Score 1194.5; DB 11; Length 383;
Best Local Similarity 58.9%; Pred. No. 4.6e-99;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;

Qy 1 MAFVCLAIGCLTYFLISTFGCTSSDTEIKVNPQDFEIVDPGVLGYLYLQWPPPLSLD 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MAFV--HRCCLCFLITCTGVS---LEIKVNPQDFEILDGLGYLYLQWPPPVVIE 54

Qy 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLKNKIEAKIHTLLPWCOTNGSEVQ 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 55 KFKGCTLEYELKYRNVDSNKTITIRNLTKGFDLKNKIEGKIRTHLSEHCTNGSEVQ 114

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Db 362 CKICHLWIKLFP 373
: : : | : |
: : : | : |

RESULT 4
Q920K4 PRELIMINARY; PRT; 415 AA.
AC Q920K4;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE INTERLEUKIN-5 RECEPTOR ALPHA PRECURSOR.
GN GFIL-5RA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Norris T.E.;
RT "Cloning and Characterization of the Guinea Pig Interleukin-5 receptor
alpha cDNA.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U55215; RAD0361.1; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003532; -.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Signal; Receptor.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA.
SQ SEQUENCE 415 AA; 46913 MW; 41BA4BA597B31CD4 CRC64;

Query Match 14.2%; Score 298.5; DB 11; Length 415;
Best Local Similarity 26.5%; Pred. No. 1.1e-18;
Matches 103; Conservative 67; Mismatches 172; Indels 47; Gaps 19;

QY 6 LAICGLYFLSTFTGCTSSDTEIKVNPQDFEIVDPGLYLQWQPLSLDHPKEC 65
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 7 ILGAIETLQDTL-----PDKRFLPLPPINFYKVTG-LAQVVLQWEPNQGQ-KNV 58
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 66 TVEYELRYNIGSETWTKITIKNHYKDGFDLNGIEAKIHTLLPWQCTNGSEVOSSWAE 125
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 59 NLNVHVKINTPQEDYE---TRNTQSKCETLHQGVASVETIL-WH--GHSLLASSWVS 112
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 126 TTYWISPOGIPETKVQDMCV-----YNNWQ----YLLCSWRKPGIGVLLDTNLYFY- 173
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 113 AEH-KAPPGSPGTSIVNLCTTNTAASNYTNLKSVEYSLHCTWLAGKADPEDTQYFLYR 171
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 174 ---WYEGLDHALQCVDIKAD-GONIGCRFP--YLEASDYKDFYICVNGSENKPIRSSY 227
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 172 YGPWTE-----ECOEYSKDTLSNTACFPFRTPIHAKDRDLAVHVGSSNHATIKPFD 225
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 228 FTFQLQNVKPLPPVYLTFTRESSECEIKLWKSIPGLPIPARCFDYETEI-REDDTLVTA 286
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 226 QLFTQALQDQNPMDVATEGS-RUSIQMKPVSAPFPIHCFEYEVKIKNTKDYQVEK 284
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 287 TVENETYLKTTNTRQLCFVRSKVNLYCSDGIGWSEWSDKQWGEDLSKTKTLR-FW 345
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 285 TTTNA--FVSTDGVSKYSIQVRAAVSPHCRAMGLWSKWS-QPYVVGKE--KPIAGWFL 339
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 346 LPFGFILLIVFTGLLLRKPNTPKMP 374
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 340 ITLPAVLFCILLIFFELCRHYHLWTKMFP 368
: : : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 5
Q15469 PRELIMINARY; PRT; 333 AA.
ID Q15469
AC Q15469;

DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSILSR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MEDLINE-92121815; PubMed-1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT "Molecular cloning and expression of the human Interleukin 5
receptor.";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL: X62156; CA44081.1; -.
DR InterPro: IPR002996; -.
DR InterPro: IPR003532; -.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;

Query Match 13.9%; Score 292; DB 4; Length 333;
Best Local Similarity 28.0%; Pred. No. 3.2e-18;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

QY 27 DTEIKVNPQDFEIVDPGLYLQWQPLSLDHPKECTVEYELKYRNISETWTKIIT 86
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 25 DEKISLLPPVNETIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAKPKEDDYETRI 82
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 87 KNLHYKDGFDLNGIEAKIHTLLPWQCTNGSEVOSSWAEITYWISPOGIPETKVQDMCV 146
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 83 ES---KCVTILHKGFSAVSRTILQ---NDHSLASSWASAEHL-APPGSPGTSIVNLCT 135
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 147 -----YNNWQYLL-CSWKPGIGVLLDTNLYFY---WYEGLDHALQCVDIKAD 191
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 136 TWTEDNYSLRSYQVSLHCTWLVGTDAPEDTQFLYRYGSWTE-----ECOEYSKDT 189
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 192 -GONIGCRFP--YLEASDYKDFYICVNGSENKPIRSSYFTFQLQNVKPLPPVYLTFT 248
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 LGRNIACWFPTFLSKGRDLAVLVNGSSKHSAIRPFDQLFALHAIQINPLNVTAEI 249
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 249 ESSECEIKLWKSIPGLPIPARCFDYETEIREDDTTLVTVATVENETIYTLKTTNETRQLCFV 308
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 250 EGT-RLSIQWKEKPVSAFPIHCFDYEVKIHNTRNGLQIEKLMTNAFISIIDLSKYDVQV 308
: : : | : | : | : | : | : | : | : | : | : | : | : |

QY 309 RSKVNLYCSDGIGWSEWS 326
: : : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 RAAVSSMCREAGLWSEWS 326
: : : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 6
O97597 PRELIMINARY; PRT; 349 AA.
ID O97597
AC O97597;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN PRECURSOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.L., Hirano A., Brown W.C., Estes D.M.;
RT "Biological activities of interleukin-13 on bovine lymphocytes:

```

RT. implications for signaling through IL-13Ra1.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBDJ databases.

[illegible]

Query Match 12.6%; Score 264.5; DB 6; Length 349;
Best Local Similarity 24.4%; Pred. No. 9.9e-16;
Matches 83; Conservative 63; Mismatches 135; Indels 59; Gaps 16;

Qy	53	WOPPLSLDHFKECTVEYELKYRNI	GETWKTITTKNLHYKDGFDL	LNKGTEAKIHTLLP	QW 112	
Db	18	WNPEGAS--PNC	SLKY--F	SHFGKQDKKIA	PET--HRSKEVPLNERICLOVGS---Q 67	
Qy	113	C-TNGSEVQSSWAET	YTWISPOGIPETK	VQDMDCVYNNQYL	CLCSKPKGIGVLLDTNYNL 171	
Db	68	CSINESEKPSIL	VEKCF-SP	PEGDPESAVTALOC	IWHNLRYMKCTWLPGRNASPDNYIL 126	
Qy	172	FYWEGLDHLALQ	VDYIKADGQNI	GRFPYLEASD--YK	DFYICVNGSSSENPIRSSYTF 229	
Db	127	YYHNSLGKTLQ	CENTFYR-EG	QHACSFNLTKV	KDSFEQHSQVQVMVRNACKISPSFNI 185	
Qy	230	FQLONIQVLP	PPLYLFTTRESSCE	IKLWSIP	LGPAPARCFDEYIEIRDDTTLVTATVE 289	
Db	186	VPLTSHVKP-D	PSHIRKLSFQ	NDLYVQW	TNPQN-FQSQC	LCYCEVEVINSHA----- 235
Qy	290	NEHYTLKTTN	ETNR-----Q	LCFW-----	RSKVNIYC-SDDGIWS 323	
Db	236	ETHDIFYVEE	AKQNTPEEGN	LEGTCISF	MPVGLPDTLNTVRI	RVKTKNLCYEDDKLWS 294
Qy	324	EWSDKOCW	EGEDLSK	TLRLF	WLPFGFILILV	IFVTGLLL 363
Db	295	NWS-----	QAMSGORANOT	FYIT--TLLI	IPVIVAAAVI 327	

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RESULT      7
Q9UDY5
ID          Q9UDY5      PRELIMINARY;      PRF;      279 AA.
AC          Q9UDY5;
DT          01-MAY-2000 (TREMBlrel. 13, Created)
DT          01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT          01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE          INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
OS          Homo sapiens (human)
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX          NCBI_TaxID=9606;
[1]
RN          SEQUENCE FROM N.A.
RP          Wada M., Hisano T., Kuwano M.;
RL          Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RR          EMBL: U81380; AAD00511.2; -.
DR          HSSP: P40189; 1BQU
DR          InterPro: IPR002996; -.
DR          InterPro: IPR003532; -.
DR          PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
SQ          Receptor.      279 AA; 31658 MW; E74141FE9F8E9BB CRC64;
KW

```

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Query Match      11.5%; Score 241.5; DB 4; Length 279;
Best Local Similarity 27.%; Pred. No. 8.6e-14;
Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;

QY 11 LYTLFLSTTTGCTSSSDTEIKVNPQQDFEIVDPGYGLYXLQWPPSLDHFKECTVEY - 69
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
10 LWAALLCAGGGGGGGGAAPETQPTVNTLSVSVENLCTVITWNNPPGAS--SNCSLWIF 67
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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Query Match          9.4%; Score 197.5; DB 13; Length 363;
Best Local Similarity 21.9%; Pred. No. 1.1e-09;
Matches 61; Conservative 56; Mismatches 134; Indels 27; Gaps
QY 97 LNKGIKAIITPLPWQCTNGSEVQSSWAETTYWISQGIPETKVQDMQCVYVNWQYLCLS 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 IHKYVRVELVTLIPTVHFDMKVGSW--LFLLSLQGYEAPSTPNVNLGIIINLDYVNCI 58
QY 157 WKPGIGVLLDTNYNLFVWYEGLDHALQCVDYIKADQNTIGCRPEYLEASDYKDFYICVNG 216
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 WSE--QSIPEVNTFTFSRFIKONMEECTYTLQGEASYAVGCLSYDKSDRFR----- 108
QY 217 SSENKPRSSRVFTFQ---LQNIKVPPLPVVLTFTRESSCEIKLKWSIPLGPIPARCFDYE 273
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 109 TLKTKLVHQNYSYVDHNLKSMVKLPPVNLSEVMKDPDLNLYWNNKNTF---CIESE 165
QY 274 IEIREDDTTLVATVENE-TYTLKTTNETRQLQCFVVRKVNIVCYSDDGJWSEMSDKQWCE 332
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 166 VRYRINSDKKWKTSPSKEQKVAEFLKSSRYEFQVRARVNDMCGSEFWSEWSQPIQWD 225
QY 333 G-----EDLSKTKLIRFWLP-RGFILILVIFVTGLLL 363
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 226 SMKGNNTIDTSGSS-MSVWKPVLSLGTWTLFTLACLML 262

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RESULT	9	
Q9PT10		
ID	Q9PT10	PRELIMINARY;
AC	Q9PT10;	PRT;
DT	01-MAY-2000	611 AA.
	(TRENBLrel. 13, Created)	

RA Wang T., Secombes C.J.;
RT "Cloning and expression of the first non-mammalian cytokine receptor
RT common gamma chain gene in rainbow trout (*Oncorhynchus mykiss*).";
RL submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

```

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087225; PubMed=10618394;
RA Huang H., Brown D.B.;
RT "Prolactin is not a juvenile hormone in Xenopus laevis
RT metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL; AF193800; AAF05776.1; -.
DR HSP; P16471; I8P3
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003528; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68255 MW; 85629F91776FFB6 CRC64;

Query Match      8.9%; Score 187; DB 13; Length 611;
Best Local Similarity 26.1%; Pred. No. 1.8e-08;
Matches 70; Conservative 41; Mismatches 117; Indels 40; Gaps 11;

QY 127 TYWISPOGIPETKVQDDCVYNNQYLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCV 186
DB 22 TVSLNAQSLPGKPYID-KCRSEKVTSCWKKPGSDGGLPTNYSLLYRKENDPKIYEC 80
QY 187 YIKADGONIGCRFFYLEADSYKDYICVNGS-----SENKPIRSSYFTFQLQNI 239
DB 81 YV-TSGLN-SCFFDKAHTSEWIFHYIYVNTALNGSNVDSDESDVTY-----IV 131
QY 240 PPVYLTFRESS-CEIKLWSIPGLPIPARCFD-----YEIEIREDDTTLVTAT 289
DB 132 PPTNVSLAVESGHDLKWK-----LPPAMVDVQSGWMLTLKYEVRYKEEKEQ 185
QY 290 NETYTLKTTNETROLCFVRSKVNIGS-DDGIWSEWSKQCEGEDLSKTKLLRFLW 348
DB 186 GNQLKLLGLTLPNGNVVQ----VRCKPDSGHSEWSESTESYIPIGGKKTDLT 241
QY 349 GFI--LILVIFVTGLLRKPNTPYKMP 374
DB 242 GALSAVICLTMIWTMALKRCSLMSCILP 269

RESULT 11
Q64146 ID Q64146 PRELIMINARY; PRT; 896 AA.
AC Q64146;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
GN RIL-3R<BETA>.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370942; PubMed=7643220;
RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
RT microglia and its mRNA expression in vivo.";
RL J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-WISTAR; TISSUE-BRAIN;
RA Gebicke-Haerter P.J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; S79263; AAB35068.1; -.
DR EMBL; AJ000555; CAA04186.1; -.
DR InterPro; IPR000282; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003531; -.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Signal.
FT NON_TER 896
FT INTERPRO 896
SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

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DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087225; PubMed=10618394;
RA Huang H., Brown D.B.;
RT "Prolactin is not a juvenile hormone in Xenopus laevis
RT metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL; AF193800; AAF05776.1; -.
DR HSP; P16471; I8P3
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003528; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68255 MW; 85629F91776FFB6 CRC64;

Query Match      8.9%; Score 187; DB 13; Length 611;
Best Local Similarity 26.1%; Pred. No. 1.8e-08;
Matches 70; Conservative 41; Mismatches 117; Indels 40; Gaps 11;

QY 127 TYWISPOGIPETKVQDDCVYNNQYLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCV 186
DB 22 TVSLNAQSLPGKPYID-KCRSEKVTSCWKKPGSDGGLPTNYSLLYRKENDPKIYEC 80
QY 187 YIKADGONIGCRFFYLEADSYKDYICVNGS-----SENKPIRSSYFTFQLQNI 239
DB 81 YV-TSGLN-SCFFDKAHTSEWIFHYIYVNTALNGSNVDSDESDVTY-----IV 131
QY 240 PPVYLTFRESS-CEIKLWSIPGLPIPARCFD-----YEIEIREDDTTLVTAT 289
DB 132 PPTNVSLAVESGHDLKWK-----LPPAMVDVQSGWMLTLKYEVRYKEEKEQ 185
QY 290 NETYTLKTTNETROLCFVRSKVNIGS-DDGIWSEWSKQCEGEDLSKTKLLRFLW 348
DB 186 GNQLKLLGLTLPNGNVVQ----VRCKPDSGHSEWSESTESYIPIGGKKTDLT 241
QY 349 GFI--LILVIFVTGLLRKPNTPYKMP 374
DB 242 GALSAVICLTMIWTMALKRCSLMSCILP 269

RESULT 10
Q9IBF6 ID Q9IBF6 PRELIMINARY; PRT; 611 AA.
AC Q9IBF6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;
RT "Cloning of a cDNA for Xenopus prolactin receptor and its
RT metamorphic expression profile.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030443; BAA90400.1; -.
DR InterPro; IPR001777; -.

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Query Match      8.5%; Score 178; DB 11; Length 896;
Best Local Similarity 21.4%; Pred. No. 1.8e-07;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY 5 CLATGCL--YT-FLISTFTGCTSSDREIKVN-----PPQDEIVDPGYLGYL 49
DB 94 CVPKRCVLPYTFQFSKEDYSLQPDRLSLHLVPLAQHVQPPPKDISPSG--DHF 151
QY 50 YLQWQPLP---SLDHFECTVEYELKRNIGTSETWKTIIKNLHYKDGFDLNGIEAKIH 106
DB 152 LKWSVPLGDAQVSLLSKQDIQFEVAKQL-QDSWED--ASSLH-----TCNLWVTLEPK 203
QY 107 TLLP-----WQCTNSGEVQ---SSWAEYTWISPOGIPETKVQDMDCVYNNWYLL 154
DB 204 LFLPNSIYVARVRAQLAGSSLSGRPSGWSPEVHWDSPTE-DKARPQNLOCFDGIQSLN 262
QY 155 CSWKPFGVLLDTWYNLFYWEGLDHALQVDYIKADQONIGCRFPYLEASDYKDFYICV 214
DB 263 CSWEVWTKVTDSVSGFLFYSSPRAGEKKGSPVVK-----LQASRYTRYHCSL 311
QY 215 NGSENKPIRSSYFTFOLO-----NIVKPLPP-VLTFRESSCEIKLKWISPL 262
DB 312 NVSD---PAHSQYTVSVKRLQCKFTESFNHIOQNNPTLMTKNRDS---YSLHWETQK 365
QY 263 GPIPARCFDYEIEIR-----EDDTTLVTATVENETYTLKTTNETROLCFVYRSKVNIYC 316
DB 366 MSYFFIQHAFQVQYKKLDRWEDSKT---ENLNAHSMIDLPOLEPGTSCYCARVRVKIP 421
QY 317 SDDGIWSEWSKQWEGEDLSKTLRLFWLPGFILLIVFTVGLLL 363
DB 422 EYKGLWSEWSNCTWT-TDWMVMTL---WI-----VLILVFLILFTLL 460

RESULT 12
Q9PTH9 PRELIMINARY; PRT; 611 AA.
AC Q9PTH9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE PROLACTIN RECEPTOR B.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang H., Brown D.D.;
RL MEDLINE=20087225; PubMed=10618394;
RT "Prolactin is not a juvenile hormone in Xenopus laevis
  metamorphosis."
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL; AF193801; AAF05777.1; -.
DR HSP; P16471; Ibp3.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003528; -.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68481 MW; CAC658A84A66B313 CRC64;

Query Match      8.3%; Score 174.5; DB 13; Length 611;
Best Local Similarity 26.4%; Pred. No. 2.3e-07;
Matches 68; Conservative 39; Mismatches 120; Indels 31; Gaps 11;

QY 131 SPOGIPETKVQDMDCVYNNWYLLCSKPKGIGVLLDTNLYNLFYWEGLDHALQVDYIKA 190
DB 29 SPPGKPEI-----IKRSYKVTFCWKPASDGLPTNYSLLYRKENDPKIYECPDY-ET 83

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QY 191 DGONIGCRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFQLQNIKVPPLPVY 243
DB 84 SGLN-SCYFDKAKHTSFWFVHIYVYNATLGSNNVSELSVDITY-----IVETYPPTN 135
QY 244 LTTRESS-CEILKWSIP-LGPIPA--RCFDYEIEIREDDTLVTATVENETYTLKTTN 299
DB 136 LSTVEDGHDLVLLKYPHPDMADVQSGWLTLYKEVRLKEEKEQWEAHSVGNQLKLKLYG 195
QY 300 ETROLCFVYRSKVNIYCS-DDGIWSEWSKQWEGEDLSKTLRLFWLPGFI--LILVI 356
DB 196 LTPGNNVWQ-----VRCKPDSGHWSEWSQESYTIQLGGKKTDMLMLISVGTLSAVICLT 251
QY 357 FVTGCLLRKPNTPYKMP 374
DB 252 MIWTMLKRCVSMCILP 269

RESULT 13
O57519 PRELIMINARY; PRT; 881 AA.
AC O57519;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE GP130P1.
DE GP130P1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC09531.1; -.
DR HSP; P40189; IBOU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003529; -.
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D21138A0 CRC64;

Query Match      8.2%; Score 173.5; DB 13; Length 881;
Best Local Similarity 25.0%; Pred. No. 4.5e-07;
Matches 75; Conservative 37; Mismatches 115; Indels 73; Gaps 14;

QY 68 EYELKYRNIGSETWKTIIKNLHYKDGFDLNGIEAKIHLLPWCQINGSEVQSSWAETT 127
DB 74 QYELNQTSSVTFFENLTLLN-----SPLTCNVNASHV-----ANTL 111
QY 128 YWI-SPOGIPETKVQDMDCVYNNWYLLCSKPKGIGVLLDTNLYNLFY-W-YEGLDHALQC 184
DB 112 YGIFFTLGLPDKPTNLTCIVYNQDNLCTWDPCRPNTLPTNYTLSHRWAHFGANY---- 167
QY 185 VDIKADQONIGCRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQLQNIKVPPLPVY- 243
DB 168 -----CRGANNSTIHSPPGFQYIDTTFQVEATNELGIQKSETLIDPVNIVKPNPQLS 222
QY 244 -LTTRESSCEILKWSIPLGPI-----PARCFDYEIEIREDDTLVTATVENET 292
DB 223 ELISSLELPLNALKIEWKNPITNAPLNKYNIRYRPVKTDWEM-VPEEDT-----ASRDS 276
QY 293 YTLK-----TTNETROLCFVYRSKVNIYCSDDGIWSEWS--KQCW-----EGEDLSK 339
DB 277 FTLDLPLNTVIEVSIRC-----LHKDGHGFWSDWSLKKQVTEAPPSPRGPDWKK 328

RESULT 14

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Q921A0 PRELIMINARY; PRT; 890 AA.

AC Q921A0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR BETA CHAIN.
GN IL5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;

SEQUENCE FROM N.A.
RA Logsdon N.J., Graham A., Scott C.W.;
RT "Guinea pig IL5 receptor beta chain."
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U94688; AAC77520.1; -
DR InterPro; IPR000276; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003531; -
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 890 AA; 96578 MW; D43FB1CA88525536 CRC64;

Query Match 8.1%; Score 170; DB 11; Length 890;
Best Local Similarity 23.8%; Pred. No. 9.4e-07;
Matches 88; Conservative 53; Mismatches 144; Indels 84; Gaps 21;

Qy 34 PPQDFEIVDPGLYLILQWQPLSLDH---FKECTVEYELKYRNIGSETWKTITIKNLH 90
Db 138 PPQDVQINTSG--DQVLLTWSVALEGPHTSWLSQRLDEFEVYKRL-HEPWESAST--LH 192
Qy 91 YKDG-----FDLKGIEAKIHITLLPWQCTNGSEVO---SSWAETTYWISPGQIPETK 139
Db 193 SNSSOALGPELFLPSSYIVARVTRL---ARGSGFSRPSQMSPEVSWSSQPG-DQAQ 247
Qy 140 VQDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDHALQ-CVDYIKADGONI--- 195
Db 248 PQNLQCVFDGARTLCSWEVRSQVTSVSGFLY-RSSLDAGEQECPOVQKEELHDIYTR 306
Qy 196 -GCRPPYLEADYKDFYICVNGSSENKPIRSYFTFQLNIVKPLPPVYLFTRESSCEI 254
Db 307 HSCQIRVSNRPHSQYTVTRPNRGEKFIKSA-----NHIQMAAPT-LNVTKDGD-TY 357
Qy 255 KLKWSIPLGPIPARCF-----DYEIEIREDDTLTATVENETVTLK----- 296
Db 358 SLRW-----VTEKMYSHIENTEIQYR---TAGDRWENSKTETLKNAHNMPPLPLEP 407
Qy 297 -TTNETROLCFVWRKSVNIYSDPGINSEWSKQWGEDLSKTKLLRFW-LPFGFILIL 354
Db 408 ATTLYAR-----VRVKPSGPGAYNGINSEWSEQRWTTD-----WALPTWVLALV 452
Qy 355 VIFVTGLILL 363
Db 453 LVLVTLALL 461

RESULT 15
Q9N0J7

ID Q9N0J7 PRELIMINARY; PRT; 622 AA.
AC Q9N0J7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Dairymple A., Edery M., Jabbour H.;
RT "Sequence and functional characterisation of the marmoset monkey
RT (Callithrix jacchus) prolactin receptor: comparative homology with the
RT human long form prolactin receptor."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ272217; CAB75847.1; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal; Receptor.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 622 PROLACTIN RECEPTOR.
SQ SEQUENCE 622 AA; 69425 MW; 65F99522C6CD6DB6 CRC64;

Query Match 7.9%; Score 167; DB 6; Length 622;
Best Local Similarity 28.8%; Pred. No. 1.1e-06;
Matches 61; Conservative 26; Mismatches 91; Indels 34; Gaps 10;

Qy 131 SPQGIPTKVDMDCVYNNQYLLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCVDIKA 190
Db 26 SPQKPEI----FKCRSPNKETFTCWWRPGADGGGLPTNLSLAYHKEGKFTHECPDYV-T 80
Qy 191 DQONIGCRFPYLEASDYKDFYICVNGSSENKPIRSYFTFQLNIVKPLPPVYLFTTRES 250
Db 81 GGPN-SCHFGKQYTSWRTYITVNTATNMGSTLSDEIYVDVTIVEPDPPLNVV----- 134
Qy 251 SCEIK-----LKWSIP-LGPIPARCFD--YEIEIREDDTLTATVENETVTLKT 297
Db 135 -VEYKQPEDKPKYLMKIRKSPPTLIDLKTGWFTLLYEIQLKPENAE-----EWETHFAGQ 187
Qy 298 TNETROLCFVVRSK--VNIYCS-DDGIWSEWS 326
Db 188 QTFKVLSLHFGQKYLQVQCKPDHGYWSSWS 219

Search completed: September 1, 2001, 19:15:52
Job time: 524 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:55 ; Search time 43.66 seconds
(without alignments)
587.971 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_337

Perfect score: 1873

Sequence: 1 MAFVCLAIGCLYFLISTTF.....DDGIWSEWSKQWEGEDLS 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	293.5	15.7	420	2 S21052	interleukin-5 rece
2	292	15.6	335	2 A40267	interleukin-5 rece
3	254	13.6	831	2 JQ1655	prolactin receptor
4	229	12.2	415	2 S12357	interleukin-5 rece
5	210.5	11.2	830	2 I50455	prolactin receptor
6	202.5	10.8	369	2 A42565	interleukin-2 rece
7	199.5	10.7	373	2 A55718	interleukin-2 rece
8	198.5	10.6	369	2 I49280	interleukin-2 rece
9	179	9.6	878	1 A40091	interleukin-3 rece
10	165	8.8	310	2 A29884	prolactin receptor
11	165	8.8	412	2 A41070	prolactin receptor
12	165	8.8	581	2 I45971	prolactin receptor
13	165	8.8	610	2 A34631	lactogen receptor
14	165	8.8	610	2 A36116	prolactin receptor
15	165	8.8	896	2 I56563	interleukin-3 rece
16	160	8.5	897	1 A39255	cytokine receptor
17	159	8.5	292	2 I77525	prolactin receptor
18	159	8.5	303	2 I77524	prolactin receptor
19	159	8.5	608	2 I53269	prolactin receptor
20	155.5	8.3	896	1 A35782	cytokine receptor
21	151	8.1	622	2 A40144	prolactin receptor
22	150.5	8.0	917	2 I49699	glycoprotein 130 -
23	147	7.8	616	2 A30304	prolactin receptor
24	133.5	7.1	333	2 S13684	granulocyte-macrop
25	133.5	7.1	378	2 S50040	granulocyte-macrop
26	133.5	7.1	400	2 S06945	granulocyte-macrop
27	130.5	7.0	378	2 A40266	interleukin-3 rece
28	129	6.9	150	2 B34631	lactogen receptor
29	128	6.8	630	2 I51086	prolactin receptor

ALIGNMENTS

RESULT 1

S21052

Interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence.revision 10-Nov-1995 #text.change 01-Dec-2000

C;Accession: S21052; S21050: S21053; A46175; S78106; S78107

R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.

J. Exp. Med. 175, 341-351, 1992

A;Title: Molecular cloning and expression of the human interleukin 5 receptor.

A;Reference number: S21050; MUID:92121815

A;Accession: S21052

A;Molecule type: DNA

A;Residues: 1-420 <MUR>

A;Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844

A;Experimental source: clone lambda h5R.12

A;Accession: S21050

A;Molecule type: DNA

A;Residues: 1-395, 'I' <MU2>

A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840

A;Experimental source: clone lambda h5R.27

A;Accession: S21053

A;Molecule type: mRNA

A;Residues: 1-332, 'K' <MU3>

A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466

A;Experimental source: clone lambda h5R.25

R;Ravener, J.; Tsupens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.

Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992

A;Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum

A;Reference number: A46175; MUID:92357767

A;Accession: A46175

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 333-420 <TAV>

A;Experimental source: HL-60 cells and eosinophils

A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)

R;Murata, Y.

Submitted to the EMBL Data Library, July 1991

A;Reference number: S78106

A;Accession: S78106

A;Molecule type: DNA

A;Residues: 1-128, 'I', 130-395, 'I' <MUW>

A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840

R;Murata, Y.

Submitted to the EMBL Data Library, September 1991

A;Reference number: S78107

A;Accession: S78107

A;Molecule type: mRNA

A;Residues: 1-128, 'I', 130-332, 'K' <MU4>

A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466

C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>

F:345-365/Domain: transmembrane #status predicted <TM>
F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.78; Score 293.5; DB 2; Length 420;
Best Local Similarity 28.18; Pred. No. 4.2e-16;
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps 13;

Qy 27 DTEIKVNPQDFEIVDPGYLYLQWOPPLSLDHFECTVEYELKYRNGISGSETWKTIIT 86
Db 25 DEKISLLPPVNFITKVYG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
Qy 87 KNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETIYISPOGIPETKVDMDCV 146
Db 83 ES---KCVTLHKGFSAVSRTILQ---NDHSLASSWASAEHL-APPGSPGTSVNLNCT 135
Qy 147 -----YNNQYLL-CSWKGIGVLLDTNLYFY---WTEGLDHALQCVDIKAD 191
Db 136 TMTEDNYSLRSYQVSLHCTWLVTGTDAPETQYFLYRYGSWTE-----ECOEYSKDT 189
Qy 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVLTFTFR 248
Db 190 LGRNIACWFPRTFILSGRWLAVLVNGSSKHSAIRPDFQALFALHAIQDQINPLNVTAEI 249
Qy 249 ESSCEIKLWSIPLGPIPARCFDYEIREDDTTLVATVENETIYTKTNETRQLCFVV 308
Db 250 EGT-RLSQWEKPVSAFPIHCFDYEYKIHNRNGYLQIEKLTNAFISIIDLSKYDVQV 308
Qy 309 RSKVNIYCSDDGIWSESDKOCWEGED 335
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGN 334

RESULT 2
A40267
interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C:Accession: A40267
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers, W.; Pl
Cell 66, 1175-1184, 1991
A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
A:Reference number: A40267; MUID:92005669
A:Accession: A40267
A:Molecule type: mRNA
A:Residues: 1-335 <TAV>
A:Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
C:Keywords: cytokine receptor; transmembrane protein

Query Match 15.6%; Score 292; DB 2; Length 335;
Best Local Similarity 28.0%; Pred. No. 4.2e-16;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

Qy 27 DTEIKVNPQDFEIVDPGYLYLQWOPPLSLDHFECTVEYELKYRNGISGSETWKTIIT 86
Db 25 DEKISLLPPVNFITKVYG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT 82
Qy 87 KNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETIYISPOGIPETKVDMDCV 146
Db 83 ES---KCVTLHKGFSAVSRTILQ---NDHSLASSWASAEHL-APPGSPGTSVNLNCT 135
Qy 147 -----YNNQYLL-CSWKGIGVLLDTNLYFY---WTEGLDHALQCVDIKAD 191
Db 136 TMTEDNYSLRSYQVSLHCTWLVTGTDAPETQYFLYRYGSWTE-----ECOEYSKDT 189
Qy 192 -GONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVLTFTFR 248
Db 190 LGRNIACWFPRTFILSGRWLAVLVNGSSKHSAIRPDFQALFALHAIQDQINPLNVTAEI 249
Qy 249 ESSCEIKLWSIPLGPIPARCFDYEIREDDTTLVATVENETIYTKTNETRQLCFVV 308
Db 250 EGT-RLSQWEKPVSAFPIHCFDYEYKIHNRNGYLQIEKLTNAFISIIDLSKYDVQV 308

Db 250 EGT-RLSQWEKPVSAFPIHCFDYEYKIHNRNGYLQIEKLTNAFISIIDLSKYDVQV 308
Qy 309 RSKVNIYCSDDGIWSEWS 326
Db 309 RAAVSSMCREAGLWSEWS 326
RESULT 3
JQ1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: JQ1655; MUID:93075121
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A:Experimental source: kidney
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRSL>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 13.6%; Score 254; DB 2; Length 831;
Best Local Similarity 27.3%; Pred. No. 1.5e-12;
Matches 93; Conservative 48; Mismatches 158; Indels 42; Gaps 14;

Qy 18 TTFGCTSSDTEIKVN--PPQDFE---IVDPG-----YLGYYLQWQPLSL 59
Db 97 TTNITVTATNEICNSSDDQYVDVTSIVQSPVNLTLTKRSANIMYLAKWSPFLA 156
Qy 60 DHKECTVEYELKYRNGISGSETWKTIITKNLHYKGFDLNKGIEAKIHTLLPWQCTNGSEV 119
Db 157 DASSNHLHYELRIKPEKEEWETI---SVGVQTCQKINR-LNAGMYVYVQVRCITLDPGE 212
Qy 120 QSSWAETIYISPOG-IPETKVDMDCVYNNWOYLLCSWKGIGVLLDTNLYFYWYEG 178
Db 213 WSESSERHLLIPSGQSPPEKPTIIRKSPKEFTTCWWRPGLDGGHTNTLLYSKEGE 272
Qy 179 DHALQCVDIKADQONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQNLQIVK 238
Db 273 EQVVECPDY-RTAGPN-SCYFDKKHTSEFTIYNTVTRATNEMSGNSSDPHYVDVYIVQ 330
Qy 239 LPPVLTFTRESCEIK----LWS-IPLPPIPARCFDYEIEIR---EDDTTLVATVEN 290
Db 331 DPPVNVTLKPKINRKPYPYLVTWSPPLADVRSGWLTLEYELRLKPEGEWEWETIFVQ 390
Qy 291 ET-YTLKTTNETQLCFVVRKSVNIYCSDD--GIWSEWSDK 328
Db 391 QTOYKMFSLNPGKKYI-----IQIHKCPDHHGWSWSEWS 425

RESULT 4
S12357
interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S12357
R:Takaki, S.; Tomioka, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu
EMBO J. 9, 4367-4374, 1990
A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A:Reference number: S12357; MUID:91092260
A:Accession: S12357
A>Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-415 <TAK>
A:Cross-references: GB:D90205; NID:G220465; PIDN:BAAL4231.1; PID:G220466
C:Keywords: cytokine receptor; transmembrane protein

Query Match 12.2%; Score 229; DB 2; Length 415;
Best Local Similarity 24.8%; Pred. No. 6.4e-11;
Matches 79; Conservative 56; Mismatches 135; Indels 48; Gaps 13;

Qy 34 PPQDFEIVDPGYLYLYLOWPPISLDHFKECTVEYELKYNIGSETWTKTITNLNHYKD 93
Db 29 PVNFTIKATG-LAQVLLHDPNPQDEQ-RHVDLEYHVKINAPQDEYDTRKTES---KC 83
Qy 94 GFDLNGTEAKIHTLLPQCINGSEVQSSWAETTYWISPOGIPETKVKQDMCVYN---- 149
Db 84 VTLPHGFAASVRTLK---SSHDTLASSWSAEL-KAPPGSPGTSTVNLCTHTTVVSS 139
Qy 150 -----WQY-LICSWKPGIGVLLDTNLYLFYWEGLDHALQCVDYIK-ADGONIGCRPP- 200
Db 140 HTHLRPPYOVSLRCLWLVCKDAPEDTQYLYYRFGVLTE--KCQEYSRDLNLRNTACWFR 197
Qy 201 YLEASDYKDYICVNGSENKPIRSSTFTFQLOINVKPLPPVYLTFTRRESSCEIKLWKS 259
Db 198 TFINSKGEQLAVHINGSKRAAIKPFQLESPLAIDQVNPNNVTVEISN-SLYIQWE 256
Qy 260 IPLGPAPARCDFYEIREDD-----TTLVTATVENETTYTLKTTNETRQLCFV 308
Db 257 KPLSAPPDHCENYELKIYNTKNGHIQEKLIANKPIFISKIDVSTYSIQ-----V 305
Qy 309 RSKVNIYCSDDGIWSEWS 326
Db 306 RAAVSSPCRMFGRGEWS 323

RESULT 5
150455
prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C:Accession: 150455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: 150455; MUID:94283267
A:Accession: 150455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: EMBL:U07694; NID:G466381; PIDN:AAA20646.1; PID:G466382
C:Superfamily: cytokine receptor homology
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 11.2%; Score 210.5; DB 2; Length 830;
Best Local Similarity 24.7%; Pred. No. 4.8e-09;
Matches 86; Conservative 47; Mismatches 156; Indels 59; Gaps 14;

Qy 18 TFGCTSSSDTEIKVNPQDFEIVDPGYLG-----DPQVVDVTSIVQDPAPVNLSTKTSASTVYLLAKW 150
Db 97 TTYNTVMAINEIGSNSS-----DPQVVDVTSIVQDPAPVNLSTKTSASTVYLLAKW 150
Qy 54 QPPLSLDFHFKECTV-EYELKRYNTGSETWTKTITNLNHYKDGFDLNGTEAKIHTLLPQ 112
Db 151 SPPPLADVTSNHYRYELRLKPEKEWETV---SVGQYQYKYNR-LOAGVKYVQVVR 206
Qy 113 CTNGSEVQSSWAETTYWISPOG-IPETKVKQDMCVYNWVLLCSKPGIGVLLDTNVL 171
Db 207 CVLDTGSEWSERRHIHPNGESPPEKPTTIKCRSPEKETFTCMWPKSGDGGHPNTTL 266
Qy 172 FYWYEGLDHALQCVDYIKADQNGICRPPYLEASDYKDFYICVNGSSSENKPIRSSTFT 231

Db 267 LYSKEGEERVVECPDY-KTAGPN-SCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLVYD 324
Qy 232 LQNIKVLPPVYLYFTRESSCEIK-----LKWS-ITLGPIPA--RCFDYEIREDTITLY 284
Db 325 VTYIVQTDPPVNVTLKTKTYNRRPYLVLTWSPPPLADVRSGWLTLDYELRLKPEEA--- 381
Qy 285 TATVENETTYTLKTTNETRQLCFV-----RSKVNIYCSDD--GIWSEWS 326
Db 382 -----EWEETIFVQOQTHYKMFSLNPGKKYIVQIHKRDPDHGWSSEWS 424

RESULT 6
A42565
interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A42565; PID:G46591; I54332
R:Takeishi, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H
Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; MUID:92335883
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TAK>
A:Cross-references: GB:D11086; NID:G303611; PIDN:BAA01857.1; PID:G219890
A:Experimental source: MO1T beta lymphoid cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109167)
R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; MUID:93293887
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:L12183; NID:G307056; PIDN:AAA59145.1; PID:G307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.;
Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-11
A:Reference number: 154332; MUID:94004847
A:Accession: 154332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:L19546; NID:G349631; PIDN:AAC37524.1; PID:G349632
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1; IMD4
A:Cross-references: GDB:134807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A:Note: defects are associated with an X-linked form of severe combined immunodeficie
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

Query Match 10.8%; Score 202.5; DB 2; Length 369;
Best Local Similarity 24.8%; Pred. No. 7.4e-09;
Matches 61; Conservative 45; Mismatches 111; Indels 29; Gaps 9;

Qy 97 LNKGTAKIHTLLPQCINGSE-VQSSWAETTYWISPOGIPETKVKQDMCVYNWVLLC 155
Db 19 LGVGLNTILT-----PNGNEDTTADFFLTMPDLSVSTLPLPEVQCFFVVEYVNC 72
Qy 156 SW-----KPGIGVLLDTNLYLFYWEGLD--ALQCVDYIKADQNGICRPPYLEASDY 207
Db 73 TWNSSEPOPP-----TNLTLYHWYKNSDNDKVKCSHYLFSSEITSGCQLQKKEIHL 125
Qy 208 KDFYICVNGSSSENKPIRSSTFTFQLOINVKPLPPVYLTFTRRESSCEIKLWKSIPGP 267
Db 126 QTFVYQLQDPRE--PRQATQMLKLNVLIPWAPENLTLLHKLSEOLELNWN---NRLN 180
Qy 268 RCFDYEIRED-DTTLVTATVE-NETTYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEW 325

Db 181 HCLEHLVQRTDWDHSHWTEQSVYDRHKFSLPVDCQKRYTFVRSRFNPVLCGSAQHWSW 240
QY 326 SDKQW 331
Db 241 SHPIHW 246
RESULT 7
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KOB>
A:Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <KOB>
A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
R:Chiu, R.K.; Dougherty, G.J.
Submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma chain
A:Reference number: S37582
A:Accession: S37582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:Cross-references: EMBL:X75337
R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de
Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosoma
A:Reference number: I53398; MUID:95104285
A:Accession: I53398
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
C:Genetics:
A:Gene: IL-2Rgamma
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
A:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), bet
eptors.
C:Function:
A:Description: receptor for interleukin-2
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
C:Superfamily: interleukin-2 receptor gamma chain
F:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-369/product: interleukin-2 receptor gamma chain #status predicted <MAT>
F:256-284/Domain: transmembrane #status predicted <TM>
F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 10.78; Score 199.5; DB 2; Length 373;
Best Local Similarity 26.98; Pred. No. 1.3e-08;
Matches 63; Conservative 40; Mismatches 96; Indels 35; Gaps 10;
QY 115 NGSE-----VQSSWAETTYWISPOGIPETKQVDMDCVYNNWOYLCSW-----KPGI 161
Db 31 NGNEDITDFELTATPSET---LSVSSLPLPEVQ---CFVENVEYMNCTWNSSEPRP-- 82
QY 162 GVLDTNLYFWYEG--DHALQCVYIKADGONIGCRFFYLEASDYKDFYICVNGSSE 219
Db 83 -----TNLTLYHYKNSNDKRVQCGHYFREVTAQWLQKEITHLYETVTVQLRDPRE 137
QY 220 NKPIRSSVFTFQONIVKPLPPVLTFTRESSCEIKLKWSTPLGPIPARCFDYIEIRED 279
Db 138 --PRQSTQKQLKQNLVPAWENLTNLNLSQLELSWS---NRHLDHCLHEHVYVQVRSD 192
QY 280 -DTLVATVENE-ETYLTKTNETRQLCFVVRSKVNIYCSDDGIWSEWSKQCV 331
Db 193 WDRSWTEQSVDRHSFSLPSVDGQKFTYFVRYSRNPVLCGSAQWSEWSPHWH 246
RESULT 8
Interleukin-2 receptor gamma chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R:Caio, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) g
A:Reference number: A47514; MUID:93391374
A:Accession: I49280
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <CAO>
A:Cross-references: EMBL:U21795; NID:g727349; PIDN:AAA64279.1; PID:g727350
A:Accession: A47514
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of func
A:Reference number: JN0592; MUID:93277575
A:Accession: JN0592

A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KUM>
A:Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <KOB>
A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
R:Chiu, R.K.; Dougherty, G.J.
Submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma cha
A:Reference number: S37582
A:Accession: S37582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:Cross-references: EMBL:X75337
R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de
Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosoma
A:Reference number: I53398; MUID:95104285
A:Accession: I53398
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
C:Genetics:
A:Gene: IL-2Rgamma
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
A:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), bet
eptors.
C:Function:
A:Description: receptor for interleukin-2
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
C:Superfamily: interleukin-2 receptor gamma chain
F:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-369/product: interleukin-2 receptor gamma chain #status predicted <MAT>
F:256-284/Domain: transmembrane #status predicted <TM>
F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 10.68; Score 198.5; DB 2; Length 369;
Best Local Similarity 26.5%; Pred. No. 1.6e-08;
Matches 54; Conservative 38; Mismatches 95; Indels 17; Gaps 7;
QY 136 PETKVQDMDCVYNNWOYLCSW-----KPGIGVLDTNLYFWYEGLDHAL--QCVDYIK 189
Db 53 PTLPLPEVQCFVFNIETMNCTWNSSEPPQA-----TNLTLYHYKVSNDNTFQECSHYLF 107
QY 190 ADGONIGCRFFYLEASDYKDFYICVNGSSENKPIRSSVFTFQONIVKPLPPVYLTFTRE 249
Db 108 SKETSCQIQKEDIQLYQYFVQL--QDQKPORRAVKQLNQLNIVPAPENLTLSNL 165
QY 250 SSEBIKLKWSIPGLPIPARCFDYIEIRED-DTTLVATVENE-TYTLKTTNETRQLCFV 307
Db 166 SESOLELRWK--SRHIKERGLQYLVQYVRNDRSWTELIVNHEPRFSLPSVDELKRYTER 223
QY 308 VRKVNICYSDDDGIWSEWSKQCV 331
Db 224 VRGRYNPICGSSQWWSKQVFW 247
RESULT 9
A40091
Interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A40091; A43022

Db 183 QTQFKVFDLPGQKYLIVQTACK---PDHGWRSWQSQESSVE 220

RESULT 12
I45971
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A>Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
A:Reference number: I45971; MUID:93246019
A:Accession: I45971
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:Genetics:
A:Gene: PRLR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 8.8%; Score 165; DB 2; Length 581;
Best Local Similarity 31.3%; Pred. No. 1.4e-05;
Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;

QY 136 PETKVQDMDCVYYNMWYLLCSWKPGICGVLLDTNNFLFYWEGLDHALQCVDYIKADGQNI 195
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 27 PPEPKLVKCRSPGKETFTTCWEPFGDGGLPTNTLYTHKEGETLIHECPDY-KTGGPN- 84
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 196 GCRRPYLEASDYDFYICVNGSENKPIRSYTFQLQNIVKPLPPVVLFTRESSCEIK 255
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 85 SCYFSKKHTSIWKMYVTVAIQMGISSSDPLYVVHYIVEPPEPANLTLELKHDPDRK 144
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 256 ----LKWSIP-LGPAPRCF--DYEIEIRDDTTLTATVENET-YFLKTTN-ETQLCF 306
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 145 PYLWIKWSPMTMDVKSGWTIIQYIIRLKEPKAT-----DWETHFTLKQTQLKFNLYP 198
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 307 VVRSKNVIVCS-DDGIWSEWS 326
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 199 GKLYLVOIRKPDPHGHWSEWS 219
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 13
A34631
lactogen receptor 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 28-Jul-2000
C:Accession: A34631
R:Zhang, R.; Buczeko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A>Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A:Reference number: A34631; MUID:90241201
A:Accession: A34631
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <ZHA>
A:Cross-references: GB:M34083; NID:g205122; PIDN:AAA79273.1; PID:g205123
A>Note: The authors translated the codon GAG for residue 533 as Gly
C:Superfamily: cytokine receptor homology
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.8%; Score 165; DB 2; Length 610;
Best Local Similarity 28.5%; Pred. No. 1.5e-05;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

QY 131 SPOGIPETKVQDMDCVYYNMWYLLCSWKPGIGVLLDTNNFLFYWEGLDHALQCVDYIKA 190
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 21 SPPEGKPEIH----KCRRSPDKETTCWNPNCTDGLPTNYSLTYSKEGKTYECPDY-KT 75
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

F:253-433/Domain: cytokine receptor homology <CRS2>

Query Match		8.8%	Score 165;	DB 2;	Length 896;
Best Local Similarity		20.5%	Pred. No. 2.4e-05;		
Matches 77;		Conservative 62;	Mismatches 156;	Indels 80;	Gaps 18;
Qy	5	CIAIGCL--YT-FLISTTFGCTSSSDTEIKVN-----PPQDFEIVDPGYLGYL	49		
Db	94	CVPRCVLPYTFQFSYKEDYISLQPDRLSIHLVPLAQHVQPPPKDISISPSG--DHF	151		
Qy	50	YLQWQPPPL---SLDHFEKCTVEYELKYRNIGSETWKTITITKNLHYKDGFDLKNKGIEAKIH	106		
Db	152	LKWSVPLGDAQVLSLSQKDIQFEVAYKQL-QDSWED--ASSLH-----TCNLWVTLEPK	203		
Qy	107	TLIP-----WQCTNGSEVQ---SSWAETTYWISPOGIPETKVDQMDCVYYHNQYLL	154		
Db	204	LFLPNSIYVARVRAQLAPGSSLGRPSGWSPEVHWDSPTD-KARPQNLQCFDFGIQSLN	262		
Qy	155	CSWKFGIGVLLDTNLYFYWYEGLDHALQCVDYIKADQGNIGCRPPYLEASDYKDFYICV	214		
Db	263	CSWEVWTRVTDVSFGLFYSSSPRAGERKCSPPVKE-----LQASRYTRYHCSL	311		
Qy	215	NGSSENKPIRSYFTFQLQ-----NIVKPLPP-VYLTFPRESCEIKLKWISPL	262		
Db	312	NVSD---PAAHSQYTVSVKRLQEQGFIESFNHIQMNPTLNLTKNRDS---YSLHWETQK	365		
Qy	263	GPIPARCFDYETEIR-----EDDTLTATVAENETITLKTNETRQLCFVVRSKVNIYC	316		
Db	366	MSYPTIQHAFQVQYKKKLDWRWEDSKT-----ENLNHAHSMDLFQLEPGTSYCARVRVKTIP	421		
Qy	317	SDDGIWSEWSDKQCW	331		
Db	422	EYKGLWSEWSNECTW	436		

Search completed: September 1, 2001, 19:07:57
Job time: 124 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:15:54 ; Search time 68.62 Seconds
(without alignments)
649.764 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_337

Perfect score: 1873

Sequence: 1 MAFVCLAIGCLYFLISTTF.....DDGINSWSDKQCWEGEDLS 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_unclassified.*

13: sp_vertebrate.*

14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1184	63.2	383	11	O88786
2	293.5	15.7	420	4	Q14633
3	292.5	15.6	396	4	Q14631
4	292	15.6	333	4	Q15489
5	284.5	15.2	415	11	Q920K4
6	260	13.9	349	6	O97597
7	241.5	12.9	279	4	Q9UDY5
8	190.5	10.2	363	13	Q9DEQ1
9	170.5	9.1	881	13	O57519
10	167	8.9	622	6	Q9N0J7
11	165	8.8	296	6	O18880
12	165	8.8	611	13	Q9PTI0
13	165	8.8	611	13	Q9IBF6
14	165	8.8	896	11	O64146
15	159.5	8.5	890	11	Q921A0
16	159	8.5	227	6	Q9GLW3
17	157	8.4	581	6	O46561
18	156	8.3	625	6	Q9XS92
19	154.5	8.2	611	13	Q9PTH9

20 151 8.1 206 4 Q16354
21 151 8.1 349 4 Q9UJ5
22 147.5 7.9 538 13 Q9DFU0
23 146.5 7.8 422 4 Q9UHS
24 145.5 7.8 422 4 Q75462
25 144 7.7 217 6 O46386
26 143.5 7.7 425 11 Q9JM58
27 143.5 7.7 918 13 Q9W6U9
28 132 7.0 346 13 Q93404
29 130.5 7.0 198 6 O18985
30 130.5 7.0 390 4 Q9UEH7
31 126.5 6.8 329 4 Q9UQ41
32 117.5 6.3 896 4 Q13594
33 117.5 6.3 906 4 Q13593
34 117.5 6.3 958 4 Q13592
35 116.5 6.2 1282 5 Q9VWE0
36 114 6.1 371 4 Q9HC73
37 114 6.1 894 6 Q9MYL1
38 114 6.1 925 6 Q9MYK9
39 114 6.1 1163 6 Q9MYL2
40 114 6.1 1194 6 Q9MYL0
41 113.5 6.1 896 4 Q92919
42 113.5 6.1 958 4 Q92920
43 113.5 6.1 1165 4 Q92921
44 109.5 5.8 26926 4 Q10466
45 109 5.8 2221 5 Q9U1M1

ALIGNMENTS

RESULT 1
ID O88786 PRELIMINARY; PRT: 383 AA.
AC O88786;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IL-13 RECEPTOR ALPHA 2.
GN IL13RA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ; TISSUE=THYMUS;
RX MEDLINE=98391042; PubMed=9725226;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,
RA Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,
RA Collins M.;
RT "The murine IL-13 receptor alpha 2: molecular cloning,
characterization, and comparison with murine IL-13 receptor alpha 1.";
RL J. Immunol. 161:2317-2324(1998).
DR EMBL; U65747; AAC33240.1; -;
DR MGD; MGI:1277954; IL13ra2.
DR InterPro; IPR002996; -;
DR InterPro; IPR003532; -;
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;

Query Match 63.2%; Score 1184; DB 11; Length 383;
Best Local Similarity 64.0%; Pred. No. 9.2e-100;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;
Oy 1 MAFVCLAIGCLYFLISTTFGCTSSSDTEIKVNPQDFEIVDPGVLYLYLQWQPLSLD 60
Db 1 MAFV--HRCCLCFLLCITGYS----LEIKVNPQDFEILDPLGLLYLYLQWQPPVIE 54
Oy 61 HFKECTVEYELKYRNIGSETWKTITIKNLHYKDGFDLKNKIEAKITHTLLPQCTNGSEVQ 120
Db 55 KFKGCTLEVELKYRNVSDSNKTIITRNLYKDGFDLKNKIEGKIRTHLSECTNGSEVQ 114

QY	121	SSWAETTYWISPOGIPETKTVQDMDCVYYNNQYLLCSWKPGIGVLLDNTNVLNLYWVEGLDH	180
Db	115	SPWIEASYGISDEGSLETQIDMKCIYYNNQYLLVCSWKPGKTVYSDNTYTFMFVEGLDH	174
QY	181	ALOCVDYIKADGONICRPPYLEASDYKDFYICVNGSSNKPIRSSYFTFQLONIYVKPLP	240
Db	175	ALOCADYLQHDENKVGCKSLNDSSDYKOFFICVNGSSKLEPIRSSYFTFQLONIYVKPLP	234
QY	241	PVYLTFRESSCEIKLWSIPLGPIPARCFDYEIREDDTTLVATVENETYTLTKTNE	300
Db	235	PEFLHSIVENSIDIRMKWSTPGGPIPRCYTYEIVIREDDISWESATDKDMKMLKERANE	294
QY	301	TROLCFWRSKVNYYCDDGINSWSDKOCWEG	333
Db	295	SEDLCFFVRCVNIYCADDGIWSEWEEECWEG	327
RESULT 2			
Q14633			
ID	Q14633	PRELIMINARY;	PRT; 420 AA.
AC	Q14633;		
DT	01-NOV-1996 (TReMBLrel. 01, Created)		
DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)		
DT	01-MAR-2001 (TReMBLrel. 16, Last annotation update)		
DE	INTERLEUKIN-5 RECEPTOR PRECURSOR.		
GN	HSIL5R.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RP	TISSUE=PERIPHERAL BLOOD;		
RA	MEDLINE=92121815; PubMed=1732409;		
RX	Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;		
RT	"Molecular cloning and expression of the human interleukin 5 receptor."		
RL	J. Exp. Med. 175:341-351(1992).		
RL	EMBL; X611176; CAA43483.1; -.		
DR	InterPro; IPR002996; -.		
DR	InterPro; IPR003532; -.		
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.		
KW	Signal.		
FT	SIGNAL	1 20	POTENTIAL.
FT	CHAIN	21 420	INTERLEUKIN-5 RECEPTOR.
SQ	SEQUENCE	420 AA; 47670 MW; 8DC56DFC8BEFF524 CRC64;	
Query Match 15.7%; Score 293.5; DB 4; Length 420;			
Best Local Similarity 28.1%; Pred. No. 1.2e-18;			
Matches 92; Conservative 57; Mismatches 143; Indels 35; Gaps			
QY	27	DTBIKYNPQDPEIVDPGYLYLQWPPSLDFHEKCTVYELKYRNIGSETWKTIT	86
Db	25	DEKISLLPWNFTIKVTG-LAQVLLQWPNPQEQ-RNVNLEYQVKINAPKDEDDYETIT	82
QY	87	KNLHYKDGFDLANKGEAKTHTLLPQCTNGSWQSSWAETTYWISPOGIPETKVDMDCV	146
Db	83	ES---KCVTILHKGFSASVRTILO---NDHSLASWSASAEUH-APPGSGTGVNLTCT	135
QY	147	-----YYNQYLL-CSWKPGIGVLLDNTNLYF---WYEGDLHALQCVDYIKAD	191
Db	136	TNTEDNYSKLSYQVSLHCTVLGTDAPEDQYFLYRYGSWTE-----ECQEYSKDT	189
QY	192	-QNTGICRPP--YLEASDYKDFYICVNGSSNKPIRSSYFTFQLONIYVKPLPPVYLTFTR	248
Db	190	LGRNIACWPRFTIISKGRDWLAVLVNGSSKHSIRPFDQLFALHAIDQINPPLNVTAEI	249
QY	249	ESSCETKLKWSIPLGPIPARCFDYEIREDDTTLVATVENETYTLTKTNETROLCFVW	308
Db	250	EGT-RUSIQWEKPVSAFPJHCFDYEVKIHNTNGYLQIEKLMTNAFISIIDLSKYQVQ	308


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QY 53 WOPPLSLDHFKECTVEYELKYNIGSETWTKTITIKNLHYKGFDLNKGIEAKIHTLLPWQ 112
Db 18 WNPPEGAS--PNCSLKY---FHFCKQKDKIAPET-HRSKEVPLNERICLQVGS---Q 67
QY 113 C-TNGSEVQSSWAEITYWISPOGIPETKVQDMDCVYVNWYLLCSWKFGIGVLLDTNVL 171
Db 68 CSTNESEKPSILVEKCF-SPPEGDPESAVALQCIWHNLRYMKCTWLPGRNASPDNPYIL 126
QY 172 FYWYEGDLHALQCVDIKADGONICRFPYLEASD--YKDFYICVNGSSSENKPIRSSYFT 229
Db 127 YVWHSNLKILQCFNFR-EGOHIACSNLRKVKDSSEFQHSQVQVWVRDNRAGKISPSFNI 185
QY 230 FOLQNVKPLPPVYLTFRESCEIKLKWISPLGPIPARCFDYEIEIREDDTTTLVTATVE 289
Db 186 VPLTSHVXP-DPSHIKLSFQNGDLVQWNTPNQ-FQSQCLCYEVEVINSHA----- 235
QY 290 NETYTLTKTNETR-----QLCFV-----RSKVNIVC-SDDGIWS 323
Db 236 -ETHDIFYVEAKONTEFEGNLEGTICFMVPGVLPDLTNTVIRIRVKTNKLCEYEDDKLWS 294
QY 324 EWS 326
Db 295 NWS 297
RESULT 7
QY 9UDY5 PRELIMINARY; PRT; 279 AA.
AC Q9UDY5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE INTERLUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U01380; A000511.2; -
DR HSSP; P40189; IBOU.
DR InterPro; IPR002996; -
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 279 AA; 31658 MW; E74141FE9F8E9EBB CRC64;
```

```
Query Match 12.9%; Score 241.5; DB 4; Length 279;
Best Local Similarity 27.7%; Pred. No. 3.9e-14;
Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;
QY 11 LYTFLLSTFTGCTSSDTEIKVNPQDFEIDVPGVLYLYLQWOPPLSLDHFKECTVEY- 69
Db 10 LWALLCAGGGGGGGAAPTETQPPVTNLVSVENLCTVITWNPPEGAS--SNCSLWYF 67
QY 70 ----ELKVRNIGSETWTKIITIKNLHYKGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA 124
Db 68 SHFGDKQDKKIAPETRRSI-----EVLPLNERICLQVGS---QSTNESEKPSILV 114
QY 125 ETTYWIS-POGIPETKVQDMDCVYVNWYLLCSWKFGIGVLLDTNLYFWYEGDLHALQ 183
Db 115 EKC--ISPPEGDPESAVALQCIWHNLRYMKCTWLPGRNASPDNPYILYVWHSLEKITHQ 172
QY 184 CVDYIKADQNGICRFPYLEASD--YKDFYICVNGSSSENKPIRSSYFTFQIQNVKPLPP 241
Db 173 C-ENIFREGQVFGCSFDLTQKVDSSFEQHSQVQVWVRDNRAGKISPSFNIPLTSRKVPDP 231
QY 242 --VYLTFRESCEIKLKWISPLGPIPARCFDYEIEIREDDT 281
Db 232 HIKNLSFHD---DLYQVQWNPQNF1-SRCLFYEVVNNST 269
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RESULT 8
QY 9DEQ1 PRELIMINARY; PRT; 363 AA.
AC Q9DEQ1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang T., Secombes C.J.;
RT "Cloning and expression of the first non-mammalian cytokine receptor
common gamma chain gene in rainbow trout (Oncorhynchus mykiss).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276623; CAC09429.1; -
RW Receptor.
FT NON_TER
SQ SEQUENCE 363 AA; 41861 MW; DF69B2EE3EEA06D3 CRC64;
Query Match 10.2%; Score 190.5; DB 13; Length 363;
Best Local Similarity 22.9%; Pred. No. 2.4e-09;
Matches 55; Conservative 48; Mismatches 118; Indels 19; Gaps 6;
QY 97 LNKGEAKIHTLLPWQCTNGSEVQSSWAEITYWISPOGIPETKVQDMDCVYVNWYLLCS 156
Db 1 IHKVRVELVTLPIVTHFDMKMGWSW--LELLISLQGYEAPTPNPVNCILINDYVNCI 58
QY 157 WKPGIGVLLDTNLYFWYEGDLHALQCVDIKADGONICRFPYLEASDYKDFYICVNG 216
Db 59 WSE--QSIPEVNFTEFFSSRFKDNMEECTYLOEESYAVGCRLSYDKSDRFR----- 108
QY 217 SSENKPIRSSYFTFQ---LQNVKPLPPVYLTFRESCEIKLKWISPLGPIPARCFDYE 273
Db 109 TLKTKLVHQNMSYVQDHNLSKMKVLYPPVNLSEVMKNKDPENLYNNNSKNFTF---CIESE 165
QY 274 IEIREDDTTLVATVENE-TYTLKTTNETROLCFVRSKVNLYCGDDGIWSEWSKQWE 332
Db 166 VRYRNSDKWKTSPSKEQYAVAFPLKSSRYEQVQVAVNDMCGESEFSEWSQIQWD 225
RESULT 9
QY 9DEQ1 PRELIMINARY; PRT; 881 AA.
AC Q9DEQ1
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GP130P1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC03531.1; -
DR HSSP; P40189; IBOU.
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003529; -
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
```

[illegible]

DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match
Best Local Similarity 24.6%; Pred. No. 4.7e-07;
Matches 69; Conservative 36; Mismatches 110; Indels 65; Gaps 12;

QY 68 EYEKYNIGSETWKTIIITKNLHYKDGLNGIEAKIHTLLPWOCTSGSEVQSWSAEFTT 127
DB 74 QYELNQTSSVTFFENLTTLN-----SPLTCNVASGHV-----ANTL 111

QY 128 YWI-SPOGIPETKVQDMDCVVYNNQYLCSWRPGVGVLDTNYNLFY-W-YEGDLHALQC 184
DB 112 YGFIITGLLPDKPTNLTCIVNQDNLCATCWDGPRTNLPTNTLSHRWAHFGANY---- 167

QY 185 VDVIKADGNICRFPYLEASYDKDFYICVNGSSNKPIRSSYFTELQNIVKPVPVY- 243
DB 168 -----CRGANNSCTHSPPGFYIDTFQVEATNELGTOKSETLTDIPVNIVKPNPOL 222

QY 244 -LFTRESCEIKLKWSIPLGPI-----PARCFDYEIEIREDDTTLVATVENET 292
DB 223 ELISSLELNALKIEWKNITAFNAFNKYNIIRPVKTQDWEM-VPEEDT-----ASHRDS 276

QY 293 YTLK-----TTNETROLFCFVRSK--VNIYCS-DDGIINSEWS 327
DB 277 FTLDQLLPNTVYESVSIRC-----IHKGHGFWSDWSE 308

RESULT 10
Q9NOJ7 ID Q9NOJ7 PRELIMINARY; PRT; 622 AA.

AC Q9NOJ7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Dalrymple A., Edery M., Jabbour H.;
RT "Sequence and functional characterisation of the marmoset monkey
Callithrix jacchus) prolactin receptor: comparative homology with the
human long form prolactin receptor."
RL Submitted (FE8-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AJ272217; CAB75847.1; -.
DR InterPro: IPR001777; -.
DR InterPro: IPR002996; -.
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01352; HEMATOPOL_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal; Receptor.
FT SIGNAL
FT CHAIN 1 24 POTENTIAL.
FT CHAIN 25 622 PROLACTIN RECEPTOR.
SQ SEQUENCE 622 AA; 69425 MW; 65F99522C6CDDB6 CRC64;

Query Match
Best Local Similarity 28.8%; Score 167; DB 6; Length 622;
Matches 61; Conservative 26; Mismatches 91; Indels 34; Gaps 10;

QY 131 SPOGIPETKVQDMDCVVYNNQYLCSWRPGVGVLDTNYNLFYWEGLDHALQCVDIKA 190
DB 26 SPFGKEI-----FKCSRPKNETFTCWRRPGDGGLFTNYSLAYHKGEKFHECPDVY-T 80

QY 191 DGNICRFRPFLEYASDYKDFYICVNGSSNKPIRSSYFTELQNIVKPVPVYLFTRFS 250
DB 81 GGPN-SCHFGKQYTSRWRYIITVINAINMGSTLSDSIYVDVTVYIFEPDPPLNVV ---- 134

Query Match
Best Local Similarity 8.9%; Score 165; DB 6; Length 296;
Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;

QY 136 PETKVQDMDCVVYNNQYLCSWKRPBGIGVILLDTNYNLFYWEGLDHALQCVDIKADGONI 195
DB 27 PPEKPKLVKRCSPGKETFTCWEPGDGGCLPTNTLYTKHKEGETLIHCPCPY-KTGGRN- 84

QY 196 GRFPFLEYASDYKDFYICVNGSSNKPIRSSYFTELQNIVKPVPVYLFTRFSCEIK 255
DB 85 SCYFSKKHTSINKMYVITVNAINGMISSDPLYHVITYVEPEPPANLTLELKHPEDRK 144

QY 256 ---LAWSP-LGPIPAPRCF---DYEIFREDDTTLVATVENET-YTLKTN-ETPOLCF 306
DB 145 PYLWIRKSPTMTFDVKSGWFIIQYERLAPEKAT-----DWETHFLKQLKIFNLYP 198

QY 307 VRSKVNIVYCS-DDGIINSEWS 326
DB 199 GKLYLVQIRCKPDHGYWSSWS 219

RESULT 12
Q9PTIO ID Q9PTIO PRELIMINARY; PRT; 611 AA.

AC Q9PTIO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.

```
OX NCBI_TaxID=8355;
RP SEQUENCE FROM N.A.
RX MEDLINE=20087225; PubMed=10618394;
RA Huang H., Brown D.D.;
RT "prolactin is not a juvenile hormone in Xenopus laevis
RT metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL: AF193800; AAF05776.1; -
DR HSP: P16471; 1Bp3
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68255 MW; 85629F917766FFB6 CRC64;

Query Match 8.8%; Score 165; DB 13; Length 611;
Best Local Similarity 28.0%; Pred. No. 9.5e-07;
Matches 61; Conservative 28; Mismatches 91; Indels 38; Gaps 10;

QY 127 TYWISPGQIPETKVQDMDCVYNNWQYLLCSKPKGIGVLDTNYNLFYWYEGLDHALQCV 186
DB 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPGSDGGLPTNYSLLYRKENDPKIYEC 80
QY 187 YKADQNGICGRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFOLQNI 239
DB 81 YV-TSGLN-SCFFDKAHTSFWIFHYIYNATNALGNSVNSDESDVTY-----IV 131
QY 240 PPVLTFTRESS-CEIKLKWISPLGPIPARCFD-----YEIEIRDDTTLVAT 289
DB 132 PPTNVS LAVESGHDLKWK-----LPPAMVDVQSGWLTILKYEVRYKEEKEQ 185
QY 290 NETYLTKTNETRQLCFVVRSKVNIYCS-DDGIWSEWS 326
DB 186 GNQLKLFGLTGGNYVYQ-----VRCRPSDGSCHWSEWS 219

RESULT 14
Q64146
ID Q64146 PRELIMINARY; PRT; 896 AA.
AC Q64146;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
GN RIL-3<BETA>.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370942; PubMed=7643220;
RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
RT microglia and its mRNA expression in vivo.";
RL J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RA Gebicke-Haerter P.J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: S79263; AAB35068.1; -
DR EMBL: AJ000555; CAA04186.1; -
DR InterPro; IPR000282; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003531; -
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal.
FT NON_TER 1
FT NON_TER 896
SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

Query Match 8.8%; Score 165; DB 11; Length 896;
Best Local Similarity 20.5%; Pred. No. 1.5e-06;
Matches 77; Conservative 62; Mismatches 156; Indels 80; Gaps 18;

QY 5 CLATIGCL--YT-FLISITTFGCTSSSDTEIKVN-----PPQDFEIVDPGLCYL 49
DB 94 CVPRRCVLPYTFQFSVKEDYSLQPDRLSIHLVPLAQHVQPPPPKDISIPSG--DHF 151
QY 50 YLQWQPLP---SLDHFKECTVEYELKYNIGSETWTKTITIKNLHYKDGFDLNKGTEAKI 106
DB 152 LKWSVPLGDAQVSLLSQKDIQFVAYKQL-QDSWED--ASSLH-----TCNLWVLEPK 203
QY 107 TLLP-----WQCTNGSEVQ---SSAETTWISQGIPEKVDMDCVYNNWQYLL 154
```

```
OX NCBI_TaxID=8355;
RP SEQUENCE FROM N.A.
RX MEDLINE=20087225; PubMed=10618394;
RA Huang H., Brown D.D.;
RT "prolactin is not a juvenile hormone in Xenopus laevis
RT metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL: AF193800; AAF05776.1; -
DR HSP: P16471; 1Bp3
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68255 MW; 85629F917766FFB6 CRC64;

Query Match 8.8%; Score 165; DB 13; Length 611;
Best Local Similarity 28.0%; Pred. No. 9.5e-07;
Matches 61; Conservative 28; Mismatches 91; Indels 38; Gaps 10;

QY 127 TYWISPGQIPETKVQDMDCVYNNWQYLLCSKPKGIGVLDTNYNLFYWYEGLDHALQCV 186
DB 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPGSDGGLPTNYSLLYRKENDPKIYEC 80
QY 187 YKADQNGICGRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFOLQNI 239
DB 81 YV-TSGLN-SCFFDKAHTSFWIFHYIYNATNALGNSVNSDESDVTY-----IV 131
QY 240 PPVLTFTRESS-CEIKLKWISPLGPIPARCFD-----YEIEIRDDTTLVAT 289
DB 132 PPTNVS LAVESGHDLKWK-----LPPAMVDVQSGWLTILKYEVRYKEEKEQ 185
QY 290 NETYLTKTNETRQLCFVVRSKVNIYCS-DDGIWSEWS 326
DB 186 GNQLKLFGLTGGNYVYQ-----VRCRPSDGSCHWSEWS 219

RESULT 13
Q9IBF6
ID Q9IBF6 PRELIMINARY; PRT; 611 AA.
AC Q9IBF6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;
RT "Cloning of a cDNA for Xenopus prolactin receptor and its
RT metamorphic expression profile.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB030443; BAA30400.1; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 611 AA; 68315 MW; 7E0DF76F21D8CE97 CRC64;

Query Match 8.8%; Score 165; DB 13; Length 611;
Best Local Similarity 28.0%; Pred. No. 9.5e-07;
```

```
Db 204 LFLPNSIYVARVRAQLAPGSSLSGRPSGWSPEVHWDSPTE-DKARPONLQCFDGIQSLN 262
QY 155 CSWKPGIGVLLDTNLYNLFYWEGLDHALQVDYIKADGQNICRFPYLEASDYKDFYICV 214
Db 263 CSWEVMTKVTDSVSGFLFYSSSPKAGEKCSPPVKE-----LQASRYTRYHCSL 311
QY 215 NGSSENKPIRSSYFTFLOQ-----NIVKDLPP-VYLTFTRESCEIKLKWISPL 262
Db 312 NVSD---PAHSQYTVSKRLBQGFIESFNHIONNPPTLNLTKNRDS---YSLHWETQK 365
QY 263 GPIPARCFDYETIR-----EDDTTLTATVENETYLTKTNETRQLCFVVRKVNIVYC 316
Db 366 MSYPTQHAFOYQYKXKLDWRWDSKT-----ENLNHAHSMDLPOLEPGTSCARVRKTIIP 421
QY 317 SDGIGWSEWSKQCV 331
Db 422 EYKGLWSEWSNECTW 436

RESULT 15
Q921A0
ID Q921A0 PRELIMINARY; PRT; 890 AA.
AC Q921A0;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR BETA CHAIN.
GN IL5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Logsdon N.J., Graham A., Scott C.W.;
RT "Guinea pig IL5 receptor beta chain.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94688; AAC77520.1; -
DR InterPro; IPR00276; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003531; -
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 890 AA; 96578 MW; D43FBICA88525536 CRC64;
```

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Query Match 8.5%; Score 159.5; DB 11; Length 890;
Best Local Similarity 24.1%; Pred. No. 4.8e-06;
Matches 81; Conservative 47; Mismatches 135; Indels 73; Gaps 19;

QY 34 PPQDFEIVDPGYLYLQWOPPLSLDH---FKECTVEYELKYRNIGSETWTKITTKNLH 90
Db 138 PPQDVQINTSG--DQVLLTWSVALEGPHTSWLSQRDLFEVYKRL-HEPWESAST--LH 192
QY 91 YKDG-----FDLNGKIEAKIHITLLPQCINGSEVQ---SSWAETTYWISPGIPEYK 139
Db 193 SNSQAALGPELFLPSSYTVARVTRL-----ARGSGFGRPSQNSPEVSWSSQPG-DQAQ 247
QY 140 VQDMCVTYYNWQYLCSNKGIGVLLDTNLYNLFYWEGLDHALQ-CVDYIKADGONI--- 195
Db 248 PQNLQCVFDGAHTLSCSNEVRSQVTSVSGFLFY-RSSLDAGEQECPOVQKEELHDIYTR 306
QY 196 -GCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFLOQNIIVKPLPPVYLTFTRESSCEI 254
Db 307 HSCQIRVSNPRPHSQYTVTVRPNGEKFIRSA-----NHIQMAAPT-LNVTKDG-DY 357
QY 255 KKKWSIPLGPIPARCF-----DYIEIREDDTTLTATVENETYTLK----- 296
Db 358 SLRW-----VTEKMYSHIENTFEIQYR----TAGDRWENSKTETLKNAHNMLPPLPEP 407
```

```
QY 297 -TTNETRQLCFVVRKVNIVYCSDDGIGWSEWSKQCV 331
Db 408 ATTYLAR-----VRVKPSPGGAYNGIWSEWSEQRW 438
```

Search completed: September 1, 2001, 19:15:55
Job time: 527 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:54 ; Search time 43.66 Seconds
(without alignments)
598.440 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_343

Perfect score: 1901

Sequence: 1 MAFVCLAIGCLYFLISTTF.....EWSDKQCWGEDLSRKTLRL 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	294.5	15.5	420	2 S21052	interleukin-5 rece
2	292	15.4	335	2 A40267	interleukin-5 rece
3	254	13.4	831	2 JQ1655	prolactin receptor
4	229	12.0	415	2 S12357	interleukin-5 rece
5	210.5	11.1	830	2 I50455	prolactin receptor
6	208	10.9	369	2 A42565	interleukin-2 rece
7	206	10.8	373	2 A55718	interleukin-2 rece
8	198.5	10.4	369	2 I49280	interleukin-2 rece
9	179	9.4	878	1 A40091	prolactin receptor
10	165	8.7	310	2 A29884	prolactin receptor
11	165	8.7	412	2 A41070	prolactin receptor
12	165	8.7	581	2 I45971	prolactin receptor
13	165	8.7	610	2 A34631	lactogen receptor
14	165	8.7	610	2 A36116	prolactin receptor
15	165	8.7	896	2 I56363	interleukin-3 rece
16	160	8.4	897	1 A39255	cytokine receptor
17	159	8.4	292	2 I77525	prolactin receptor
18	159	8.4	303	2 I77524	prolactin receptor
19	159	8.4	608	2 I53269	cytokine receptor
20	155.5	8.2	896	1 A35782	prolactin receptor
21	151	7.9	622	2 A40144	prolactin receptor
22	150.5	7.9	917	2 I49699	glycoprotein 130 -
23	147	7.7	616	2 A30304	prolactin receptor
24	133.5	7.0	333	2 S13684	granulocyte-macrop
25	133.5	7.0	378	2 S50040	granulocyte-macrop
26	133.5	7.0	400	2 S06945	granulocyte-macrop
27	130.5	6.9	378	2 A40266	interleukin-3 rece
28	129	6.8	150	2 B34631	lactogen receptor
29	128	6.7	630	2 I51086	prolactin receptor

ALIGNMENTS

RESULT 1

S21052

Interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence.revision 10-Nov-1995 #text.change 01-Dec-2000

C;Accession: S21052; S21053; A46175; S78106; S78107

R;Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.

J. Exp. Med. 175, 341-351, 1992

A;Title: Molecular cloning and expression of the human interleukin 5 receptor.

A;Reference number: S21050; MUID:92121815

A;Accession: S21052

A;Molecule type: DNA

A;Residues: 1-420 <MUR>

A;Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844

A;Experimental source: clone lambda h5R.12

A;Accession: S21050

A;Molecule type: DNA

A;Residues: 1-395, 'I', <MU2>

A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840

A;Experimental source: clone lambda h5R.27

A;Accession: S21053

A;Molecule type: mRNA

A;Residues: 1-332, 'K', <MU3>

A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466

A;Experimental source: clone lambda h5R.25

R;Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.

Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992

A;Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum

A;Reference number: A46175; MUID:92357767

A;Accession: A46175

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 333-420 <TAV>

A;Experimental source: HL-60 cells and eosinophils

A;Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBP:116244)

R;Murata, Y.

submitted to the EMBL Data Library, July 1991

A;Reference number: S78106

A;Accession: S78106

A;Molecule type: DNA

A;Residues: 1-128, 'I', 130-395, 'I', <MUW>

A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840

R;Murata, Y.

submitted to the EMBL Data Library, September 1991

A;Reference number: S78107

A;Accession: S78107

A;Molecule type: mRNA

A;Residues: 1-128, 'I', 130-332, 'K', <MU4>

A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466

C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>

membrane glycoprot
leukemia inhibitor
granulocyte-macrop
protein-tyrosine-p
protein-tyrosine-p
interleukin-6 sign
titin - rabbit (fir
titin, cardiac mus
somatotropin recep
hypothetical prote
granulocyte colony
granulocyte colony
granulocyte colony
granulocyte colony
titin, muscle - ch
somatotropin recep

F;345-365/Domain: transmembrane #status predicted <TM>
F;35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.5%; Score 294.5; DB 2; Length 420;
Best Local Similarity 28.2%; Pred. No. 4.2e-16;
Matches 93; Conservative 57; Mismatches 145; Indels 35; Gaps 13;

```
QY 27 DTEIKVNPQDFEIVDPGILGYLYLQWQPPSLDHFKECTVEYELKYNIGSETWTKIIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLPPVNFITKVTG-LAQVLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIIT 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKGFDLNKGIEAKIHTLIPWQCTNGSEVOSSWAETTYISPOGIPETKVDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APGSPGTSVNLNCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YYNQYLL-CSWKPGIGVLDTNINLFY----WYEGLDHALQCVDIYKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TTTTETDNYSLRSLQVSLHCTWLVTGTDAPETQFLYRYGSWTE-----ECQEYSKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -GONIGCRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVILFTR 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACWFPRTFILSGRDWLAVLVNGSSKHSAIRPFDQLFALHAIQINPPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLWKSIPGLPIPARCFDYEIREDDTTLVTATVENETYLTKTNETRQLCFVV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIHNTNRNGYLQIEKLTNAFISIIDLSKYDVQV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 RSKVNIYCSDDGIWSEWSKOCWEGEDLSK 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 RAAVSSMCREAGLWSEWS-QPIYVGNDEHK 337
```

RESULT 2
A:40267
Query Match 15.4%; Score 292; DB 2; Length 335;
Best Local Similarity 28.0%; Pred. No. 5e-16;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;
interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers, W.; Pe-
Cell 66, 1175-1184, 1991
A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci-
A:Reference number: A40267; MUID:92005669
A:Accession: A40267
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <FAV>
A:Cross-references: GB:W75014; NID:g186387; PIDN:AAA36110.1; PID:g186388
C:Keywords: cytokine receptor; transmembrane protein

Query Match 15.4%; Score 292; DB 2; Length 335;
Best Local Similarity 28.0%; Pred. No. 5e-16;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

```
QY 27 DTEIKVNPQDFEIVDPGILGYLYLQWQPPSLDHFKECTVEYELKYNIGSETWTKIIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLPPVNFITKVTG-LAQVLQWKNPDQEQ-RNVNLEYQVKINAPKEDDYETRIIT 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKGFDLNKGIEAKIHTLIPWQCTNGSEVOSSWAETTYISPOGIPETKVDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSAVRILQ---NDHSLASSWASAEHL-APGSPGTSVNLNCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YYNQYLL-CSWKPGIGVLDTNINLFY----WYEGLDHALQCVDIYKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TTTTETDNYSLRSLQVSLHCTWLVTGTDAPETQFLYRYGSWTE-----ECQEYSKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -GONIGCRFP--YLEADYKDFYICVNGSSSENKPIRSYFTFQNLQIVKPLPPVILFTR 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACWFPRTFILSGRDWLAVLVNGSSKHSAIRPFDQLFALHAIQINPPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLWKSIPGLPIPARCFDYEIREDDTTLVTATVENETYLTKTNETRQLCFVV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Db 250 EGT-RLSIQWEKPVSAFPIHCFDYEVIHNTNRNGYLQIEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYCSDDGIWSEWS 326
 :
Db 309 RAAVSSMCREAGLWSEWS 326
 :
RESULT 3
QY1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
A:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: JQ1655; MUID:93075121
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A:Experimental source: kidney
A:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 13.4%; Score 254; DB 2; Length 831;
Best Local Similarity 27.3%; Pred. No. 1.8e-12;
Matches 93; Conservative 48; Mismatches 158; Indels 42; Gaps 14;

```
QY 18 TTFCTSSSTEIKVN--PPQDFE---IVDPG-----YLGYLQWQPPSL 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 97 TTFNITVATNEIGSNSDDQYVDVTISVQPGSPVNLTEKRSANIMYLWAKWSPPLA 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 DHFKECTVEYELKYNIGSETWTKIITKNLHYKDFGLNKGIEAKIHTLIPWQCTNGSEV 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 157 DASSNHLHYELRIKPEKEWETI---SVGVTQCKINR-LNAGMRVYVQVRCVLDPE 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 QSSWAETTYISPOG-IPETKVQDMQCVYINQWYLLCSWKPGIGVLDTNINLFYVWEG 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 WSESSSRHLIPSGQSPPEKPTTIKRSPEKETFTCWKAPGLDGGHPTNTLLYSKEGE 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 DHALQCVDIYKADQNLGCRFPYLYLEASDYKDFYICVNGSSSENKPIRSYFTFQNLQIVK 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 EQVYECPDY-RTAGPN-SCYFDKKHTSFYIYINIVTRATNEMSGNSDDPHVVDYIYVQ 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 239 LPVYLFTTRESSCEIK-----LKWS-IPLGPIPARCFDYEIEIR---EDDTTLTATVEN 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 331 DPPNVVTLKLPKPNRPYLVLTWSPPLADVRSGWLTLEYELRKPEGEWETIFVQ 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 ET-YLTKTTNETQLCFVVRKVNICYDD--GIWSEWSOK 328
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 391 QTYKMFSLNPGKKYI-----IQHCKPDHHSWSEWS 425
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 4
S12357
interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
R:Accession: S12357
R:Takaki, S.; Tomimaga, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu
EMBO J. 9, 4367-4374, 1990
A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A:Reference number: S12357; MUID:91092260
A:Accession: S12357
A:Status: preliminary

[illegible]

Biochem. Biophys. Res. Commun. 193, 356-363, 1993

A;Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of f

A;Reference number: JN0592; MUID:J93277575

A;Accession: JN0592

A;Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A;Residues: 1-369 <KUM>

A;Cross-references: DDBJ:D133565; NID:g303684; PIDN:BAA02760.1; PID:g303685

R; Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.

Gene 130, 303-304, 1993

A;Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.

A;Reference number: JN0775; MUID:93366191

A;Accession: JN0775

A:Molecule type: mRNA

A;Residues: 1-369 <ROB>

A;Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046

R; Chiu, R.K.; Dougherty, G.J.

submitted to the EMBL Data Library, October 1993

A;Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma chai

A;Reference number: S37582

A;Accession: S37582

A;Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-350,'S',352-366,'S',368-369 <CHI>

A;Cross-references: EMBL:X57337

R; DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de

Eur. J. Immunol. 24, 3014-3018, 1994

A;Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosoma

A;Reference number: I53398; MUID:95104285

A;Accession: I53398

A;Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A;Residues: 1-369 <RES>

A;Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555

C;Genetics:

A;Gene: IL-2Rgamma

A;Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3

C;Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), bet

eptors.

C;Function:

A;Description: receptor for interleukin-2

A;Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N

C;Superfamily: interleukin-2 receptor gamma chain

C;Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>

F;256-284/Domain: transmembrane #status predicted <TMW>

F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A40091; A43022
R:Itoh, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara, I.
Science 247, 324-327, 1990
A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene
A:Reference number: A40091; MUID: 90117145
A:Accession: A40091
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-878 <ITO>
R:Gorman, D.M.
submitted to GenBank, November 1989
A:Reference number: A43022
A:Accession: A43022
A:Molecule type: mRNA
A:Residues: 1-815, 'Q', 817-878 <GOR>
A:Cross-references: GB:M29855; NID:g198342; PIDN:AAA39295.1; PID:g309406
C:Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains
receptors.
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-878/Product: interleukin-3 receptor beta chain #status predicted <MAT>
F:23-440/Domain: extracellular #status predicted <EXT>
F:39-236/Domain: cytokine receptor homology <CRS1>
F:234-433/Domain: cytokine receptor homology <CRS2>
F:441-462/Domain: transmembrane #status predicted <TMW>
F:463-878/Domain: intracellular #status predicted <INT>

Query Match	9.43;	Score 179;	DB 1;	Length 878;
Best Local Similarity	23.1%;	Pred. No. 1.9e-06;		
Matches	75;	Conservative	56;	Mismatches 140;
			Indels	54;
			Gaps	20;

```

Qy 34 PPQFEIVDPGGLYLYLQWOPPL---SLDHFKECTVEYELKYRNIGSETWTKIITKNLH 90
Db 139 PPKDIIHISPSG-DHFLEWSVSLGDSQVSWLSKDI EFVAVYKRL-QDSWED-ASSLH 193
Qy 91 YKDGFLDKNGTEAKIHTLLP-----MQCTNGSEVQ---SSWAETTYWISPOGIPET 138
Db 194 -TSFNQW--LEPKL--FLPNSIYAARVTRLGAGSSLSGRKWSPEVHWDSPQG-DKA 247
Qy 139 KVQDMDCVYVNWQYLLGCKSWPKGIGVLLDTNLFYVWYEGLDHALQVDYIKADQONI--- 195
Db 248 QPQNLCQFFDGIQSLHCSWEVWTTQTSVSGFGLFYRSPAPAEKCSPVVKEQASVYTR 307
Qy 196 -GCRFPYLEASDYKDFYICVNGSSENKPIRSSVTFQOLQNVKPLPPVY-LTTRRESSCE 253
Db 308 YRCSLPVPEPSAHSQYVSVKHLQEQKFI-MSYVHIQME-----PPILNQTKNRDS--- 357
Qy 254 IKLAWSPGLGPAPARCFD--YEIEIREDDITLTATVEN---ETYTLKTTNTRQLCFV. 307
Db 358 YSLHWETQKIP--KYIDHTFQVQYKKKSESWKDSKSTENLGRVNSMDLPQLEPDTSYCAR 414
Qy 308 VRSK-VNIYCSDDGIWSEWSDKQCV 331
Db 415 VRVKPISDY---DGINSENSNYTW 436

RESULT 10
A29884
prolactin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C:Accession: A29884
R:Boutin, J.M.; Jollicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shiota, M.; Banville
Cell 53, 69-77, 1988
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
A:Reference number: A29884; MUID:88165059
A:Accession: A29884
A:Molecule type: mRNA

```

A:Residues: 1-310 <BOU>
C:Cross-references: GB:M19304; NID:g206364; PIDN:AAA1937.1; PID:g206365
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
F:1-19/Domain: signal sequence status predicted <SIG>
F:20-310/Product: prolactin receptor #status predicted <NAT>
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match	8.7%	Score 165;	DB 2;	Length 310;
Best Local Similarity	28.5%	Pred. No. 6.8e-06;		
Matches 63;	Conservative	24;	Mismatches 94;	Indels 40;
				Gaps 10;

Qy	131	SPQIGIPKTVQDMDCVYNNQYLLCSWKKPGIGVLLTNTNINLFWYEGDLHQAQCVDYIKA	190
Db	21	SPGKPEIH-----KCRSPDKETETCWNNPGTGDGLPTNSLATYSKEGKETTCEPDY-KT	75
Qy	191	DGQNGICRFPYLEASDYKDFYICVN-----GSSENKPIRSSYFTFQLOQNVKPLPPVILT	245
Db	76	SGPN-SCFFSKQYTSIWKYIIIVNATNQMGSSSDPL-----YVDVTYVEPEPPRNUT	129
Qy	246	F-----TRESSCEIKLWSIP-LGP1PARCFDYIEIREDDTLTTLTATVNEVITTLTNTNE	300
Db	130	LEVYQLDKKTYLLWKKSPPTITDVKTGWTFMEYER-----LAPAEAEWEIHFTGCH	182
Qy	301	TRQL-----CFVVRKVNICYSDDGIWSEWSKQOWCE	332
Db	183	QTQFKVPFDLPYGOKYLLVQTRCK---PDHGYWRSWQSESSVE	220

RESULT 11

A41070

prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 28-Jul-2000
C:Accession: A41070; I55417.
R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin receptor
A:Reference number: A41070; MUID:92041834
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALI>
A:Cross-references: GB:N74152; NID:g206389; PIDN:AAA41946.1; PID:g206390
R:O'Neal, K.D.; Yu-Lee, L.X.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
A:Reference number: I55417; MUID:95014432
A:Accession: I55417
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>

Query Match	8.7%	Score 165;	DB 2;	Length 412;
Best Local Similarity	28.5%;	Pred. No. 9.8e-06;		
Matches 63;	Conservative	24;	Mismatches 94;	Gaps 10;
			Indels 40;	

Qy	131	SPGIPETKQVDMDCVYYNNQYVLLCSWKPGIGVLLDTNTYNLFYWEGLDHALQCVDYTKA	190
Db	21	SPPKCKPEIH-----KCRSPKDEFTFCWNNPCTDGLPTNYSLATYSKEGETTVECPDY-KT	75
Qy	191	DGONIGCRPPYLEASDYKDFYICVN-----GSSENKPIRSSYFTQLQNIWKPLPPVILT	245
Db	76	SGPN-SCFFSKQVTSLWKYIITVNATNMGSSSDPL-----YDVVTYVPEPPRNIT	129
Qy	246	F-----TRESSCEIKLKWSP-LGPIPARCFDEIREDDTTLVTATVENETVTLTKTNE	300

Db 130 LEVQLKDKKTYLWVWSPPTITDVKGTWFTMEYR-----LKPEAEWEIHTFGH 182
QY 301 TRQL-----CFVVRSKVNIYCSDDGIWSEWSKQWE 332
Db 183 QTQFKVFDLPQKYLVTQTRCK---PDHGYSRWSQESSVE 220
RESULT 12
145971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
A:Reference number: I45971; MUID:93246019
A:Accession: I45971
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:Genetics:
A:Gene: PRLR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>
Query Match 8.7%; Score 165; DB 2; Length 581;
Best Local Similarity 31.3%; Pred. No. 1.5e-05;
Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;
QY 136 PETRVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYWYEGLDHALQCVYIKADQNI 195
Db 27 PPERKPLVKCRSPGKETFTCWNPCTDGLPTNYSLTYSKEGETTYECPDY-KTGGPN- 84
QY 196 GCRPPYLEASDYKDFYICVN-----GSSNKPIRSYFTFQNLNIVKPLPPVYLFTTRESCEIK 255
Db 85 SCYFSKHTSIWKVYITVNAINGSSDPLVHVHYIIVEPEPPANLTLKHPEDRK 144
QY 256 ----LKWSSIP-LGPIPARCF--DYEIREDDTTLVATVENET-YTLKTN-ETROLCP 306
Db 145 PYLWIKSPPTMTDVKGWFTIQEIRLKPEKAT-----DWETHFTLKQTLKIFNLYP 198
QY 307 VVRSKVNIYCS-DDGIWSEWS 326
Db 199 GQKYLQIRCKPDHGYSWS 219
RESULT 13
A34631
lactogen receptor 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 28-Jul-2000
C:Accession: A34631
R:Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.; Dufau, M.L.
Biochem. Biophys. Res. Commun. 168, 415-422, 1990
A:Title: Isolation and characterization of two novel rat ovarian lactogen receptor cDNA
A:Reference number: A34631; MUID:90241201
A:Accession: A34631
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <ZHA>
A:Cross-references: GB:M34083; NID:g205122; PIDN:AAA79273.1; PID:g205123
A:Note: the authors translated the codon GAG for residue 533 as Gly
C:Superfamily: cytokine receptor homology
F:31-216/Domain: cytokine receptor homology <CRS>
Query Match 8.7%; Score 165; DB 2; Length 610;
Best Local Similarity 28.5%; Pred. No. 1.6e-05;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

QY 131 SPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYWYEGLDHALQCVDIKA 190
Db 21 SPFGKPEIH-----KCRSPDKETFTCWNPCTDGLPTNYSLTYSKEGETTYECPDY-KT 75
QY 191 DQONIGCRPPYLEASDYKDFYICVN-----GSSNKPIRSYFTFQNLNIVKPLPPVYL 245
Db 76 SGNP-SCFFSKQYTSIWKYIITVNATNQMGSSSDPL-----YVDVYIIVEPEPPNLT 129
QY 246 F----TRESSCEIKLWSSIP-LGPIPARCFDYEIREDDTTLVATVENETYLKTTNE 300
Db 130 LEVQLKDKKTYLWVWSPPTITDVKGTWFTMEYR-----LKPEAEWEIHTFGH 182
QY 301 TRQL-----CFVVRSKVNIYCSDDGIWSEWSKQWE 332
Db 183 QTQFKVFDLPQKYLVTQTRCK---PDHGYSRWSQESSVE 220
RESULT 14
A36116
prolactin receptor 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 28-Jul-2000
C:Accession: A36116
R:Shirota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, M.; Endocrinol. 4, 1136-1143, 1990
A:Title: Expression of two forms of prolactin receptor in rat ovary and liver.
A:Reference number: A36116; MUID:91155946
A:Accession: A36116
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <SHI>
A:Cross-references: GB:M57668; NID:g206366; PIDN:AAA41938.1; PID:g206367; GB:M60728
C:Superfamily: cytokine receptor homology
F:31-216/Domain: cytokine receptor homology <CRS>
Query Match 8.7%; Score 165; DB 2; Length 610;
Best Local Similarity 28.5%; Pred. No. 1.6e-05;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;
QY 131 SPOGIPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNLYWYEGLDHALQCVDIKA 190
Db 21 SPFGKPEIH-----KCRSPDKETFTCWNPCTDGLPTNYSLTYSKEGETTYECPDY-KT 75
QY 191 DQONIGCRPPYLEASDYKDFYICVN-----GSSNKPIRSYFTFQNLNIVKPLPPVYL 245
Db 76 SGNP-SCFFSKQYTSIWKYIITVNATNQMGSSSDPL-----YVDVYIIVEPEPPNLT 129
QY 246 F----TRESSCEIKLWSSIP-LGPIPARCFDYEIREDDTTLVATVENETYLKTTNE 300
Db 130 LEVQLKDKKTYLWVWSPPTITDVKGTWFTMEYR-----LKPEAEWEIHTFGH 182
QY 301 TRQL-----CFVVRSKVNIYCSDDGIWSEWSKQWE 332
Db 183 QTQFKVFDLPQKYLVTQTRCK---PDHGYSRWSQESSVE 220
RESULT 15
I56563
interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56563
R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia a
A:Reference number: I56563; MUID:95370942
A:Accession: I56563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
C:Genetics:

Search completed: September 1, 2001, 19:07:55
Job time: 122 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2001, 19:16:25 ; Search time 24.79 Seconds
(without alignments)
473.967 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_343

Perfect score: 1901

Sequence: 1 MAFVCLAGICLYTFLISTTF.....EWSDKQCEGDELKTKLLR 343

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	1901	100.0	380	1	I132_HUMAN	Q14627 homo sapien
2	293.5	15.4	420	1	IL5R_HUMAN	Q01344 homo sapien
3	289.5	15.2	424	1	I131_MOUSE	O09030 mus musculus
4	285	15.0	427	1	I131_HUMAN	P78552 homo sapien
5	254	13.4	831	1	PRLR_CHICK	O04594 gallus galli
6	229	12.0	415	1	IL5R_MOUSE	P21183 mus musculus
7	228	12.0	831	1	PRLR_MELGA	Q91094 meleagris g
8	210.5	11.1	830	1	PRLR_COLLT	Q90374 columba liv
9	208	10.9	369	1	CVRG_HUMAN	P31785 homo sapien
10	206	10.8	373	1	CVRG_CANFA	P40321 canis famil
11	198.5	10.4	369	1	CVRG_MOUSE	P34902 mus musculus
12	187.5	9.9	379	1	CVRG_BOVIN	Q95118 bos taurus
13	179	9.4	878	1	IL5B_MOUSE	P26954 mus musculus
14	165	8.7	581	1	PRLR_BOVIN	Q28172 bos taurus
15	165	8.7	610	1	PRLR_RAT	P05710 rattus norv
16	160	8.4	897	1	CVRB_HUMAN	P32927 homo sapien
17	159	8.4	608	1	PRLR_MOUSE	O08501 mus musculus
18	155.5	8.2	896	1	CVRB_MOUSE	P26955 mus musculus
19	151	7.9	622	1	PRLR_HUMAN	P16471 homo sapien
20	150.5	7.9	917	1	IL6B_MOUSE	Q00560 mus musculus
21	150	7.9	581	1	PRLR_CEREL	Q28235 cervus elap
22	147	7.7	616	1	PRLR_RABIT	P14787 oryctolagus
23	145.5	7.7	862	1	I12S_HUMAN	O99665 homo sapien
24	133.5	7.0	400	1	GMCR_HUMAN	P15509 homo sapien
25	130.5	6.9	378	1	IL3R_HUMAN	P26951 homo sapien
26	128	6.7	630	1	PRLR_ORENI	Q91513 oreochromis
27	126.5	6.7	874	1	I12S_MOUSE	P93738 mus musculus
28	126.5	6.7	918	1	IL6B_HUMAN	P40189 homo sapien
29	123.5	6.5	1097	1	LIFR_HUMAN	P42702 homo sapien
30	113.5	6.0	1165	1	LEPR_HUMAN	P48357 homo sapien
31	112.5	5.9	1630	1	PTPL_DROME	P35992 drosophila
32	109.5	5.8	918	1	IL6B_RAT	P40190 rattus norv
33	107	5.6	634	1	GHR_BOVIN	P79108 bos taurus

RESULT 1
I132_HUMAN

ID I132_HUMAN STANDARD; PRT; 380 AA.

AC Q14627; O00667;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR (INTERLEUKIN-13

DE BINDING PROTEIN).

GN IL13RA2 OR IL13R.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Renal cell carcinoma;

RX MEDLINE=96279273; PubMed=8663118;

RA Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N.,

RA Ferrara P.;

RT "Cloning and characterization of a specific interleukin (IL)-13

binding protein structurally related to the IL-5 receptor alpha

chain.";

RL J. Biol. Chem. 271:16921-16926(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H.,

RA Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;

RL Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=97321053; PubMed=9177784;

RA Guo J., Apion F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;

RT "Chromosome mapping and expression of the human interleukin-13

receptor.";

RL Genomics 42:141-145(1997).

CC -!- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13

(IL-13). BUT NOT TO IL-4.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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DR EMBL; X95302; CAA64617.1; -;

DR EMBL; U70981; AAB1710.1; -;

DR EMBL; Y08768; CAA70021.1; -;

DR MIM; 300130; -;

Q28575 ovls aries
P40223 mus musculu
O99062 homo sapien
P19756 sus scrofa
Q62959 rattus norv
P48356 mus musculu
P22063 rattus norv
P26952 mus musculu
P10912 homo sapien
P08169 bos taurus
P04884 vesicular s
P70289 mus musculu

ALIGNMENTS

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DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3.1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN.
FT DOMAIN 27 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 363 POTENTIAL.
FT DOMAIN 364 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 145 155 BY SIMILARITY.
FT DISULFID 184 197
FT CARBOHYD 115 115 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B5562C887 CRC64;

Query Match 100.0%; Score 1901; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 7.1e-150;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFVCLAIGCLYTLSTFTGCTSSDTEIKVNPDPDFEIVDPGVGLYGLYQWPPPLSLD 60
Db 1 MAFVCLAIGCLYTLSTFTGCTSSDTEIKVNPDPDFEIVDPGVGLYGLYQWPPPLSLD 60

Qy 61 HFKECTVEYELKYNIGSETWKTITKLNHLKDGFDLNGKEAKIHTLLPWQCTNGSEVQ 120
Db 61 HFKECTVEYELKYNIGSETWKTITKLNHLKDGFDLNGKEAKIHTLLPWQCTNGSEVQ 120

Qy 121 SSWAETTWISPGQIPETKVDQMDCVYVNWYLLCSWKPGVGLDNTNLYFYWVEGLDH 180
Db 121 SSWAETTWISPGQIPETKVDQMDCVYVNWYLLCSWKPGVGLDNTNLYFYWVEGLDH 180

Qy 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLNIVRPLP 240
Db 181 ALQCVDYIKADQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLNIVRPLP 240

Qy 241 PVYLTFTRSSCEIKLWSIPLGPAPCFDYEIEIREDDTTLTATVENETYLTKTNE 300
Db 241 PVYLTFTRSSCEIKLWSIPLGPAPCFDYEIEIREDDTTLTATVENETYLTKTNE 300

Qy 301 TRQLCFVVRKVNICYSDGIGWSEWSDKQCEGDELKSKTLRL 343
Db 301 TRQLCFVVRKVNICYSDGIGWSEWSDKQCEGDELKSKTLRL 343

RESULT 2
ID IL5R_HUMAN
AC Q01344;
DC 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA) (CD125 ANTIGEN).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92372031; PubMed=1505961;
RA Scott H.S., Guo X.H., Hopwood J.J., Morris C.P.;
RT "Structure and sequence of the human alpha-L-iduronidase gene.";
RL Genomics 13:1311-1313(1992).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92357767; PubMed=1495999;
RA Tavernier J., Tuypens T., Plaetinck G., Verhee A., Fiers W.,
RA Devos R.;

RT RT
RL RL
RN RN
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=92005669; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuypens T., van der Heyden J.,
RA Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of
RT an IL5-specific alpha chain and a beta chain shared with the receptor
RT for GM-CSF.";
RL Cell 66:1175-1184(1991).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN
CC HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".
CC -----
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CC -----
DR EMBL; M96652; AAA59152.1; -
DR EMBL; M96651; AAA59151.1; -
DR EMBL; M75914; AAA36110.1; -
DR EMBL; A26249; CAA01793.1; -
DR EMBL; A24587; CAA01731.1; -
DR EMBL; A28251; CAA01794.1; -
DR PIR; A40267; A40267.
DR MIM; 147851; -.
DR InterPro; IPR000950; -.
DR InterPro; IPR002465; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT DOMAIN 21 342 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 343 362 POTENTIAL.
FT DOMAIN 363 420 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 333 335 NDE -> FSR (IN SOLUBLE ISOFORM S1).
FT VARSPLIC 336 420 MISSING (IN SOLUBLE ISOFORM S1).
FT VARSPLIC 333 333 N -> K (IN SOLUBLE ISOFORM S2).
FT VARSPLIC 334 420 MISSING (IN SOLUBLE ISOFORM S2).
SQ SEQUENCE 420 AA; 47700 MW; 420681FEC6B51700 CRC84;

Query Match 15.4%; Score 293.5; DB 1; Length 420;
Best Local Similarity 27.9%; Pred. No. 4.8e-17;
Matches 92; Conservative 58; Mismatches 145; Indels 35; Gaps 13;

Qy 27 DTEIKVNPDPDFEIVDPGVGLYGLYQWPPPLSLDHFKECTVEYELKYNIGSETWKTIT 86
Db 25 DEKISLLPPVNFITKVTG-LAQVLLQKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRT 82

Qy 87 KNLHYKDGFDLNGKEAKIHTLLPWQCTNGSEWSSNAETTYWISPGIPEKTKVQMDCV 146
Db 83 ES---KCVTILHKGFSASVRTILO---NDHSLASSWASAEHL-APPSPGTSIVNLTCT 135
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FT DOMAIN 25 122 FIBROBLAST TYPE-III.
FT DOMAIN 123 225 FIBROBLAST TYPE-III.
FT DOMAIN 228 325 FIBROBLAST TYPE-III.
FT DOMAIN 326 428 FIBROBLAST TYPE-III.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94102 MW; 1C4E7591DCADBE9 CRC64;

Query Match 13.48; Score 254; DB 1; Length 831;
Best Local Similarity 27.38; Pred. No. 2e-13;
Matches 93; Conservative 48; Mismatches 158; Indels 42; Gaps 14;

Qy 18 TFGCTSSDTEIKVN--PPQDFE---IVDPG-----YLGVLVQWQPLSL 59
Db 97 TTFNITVTATNEIGSSDPQYVDVTSIQPGSPVNLTLTKRSANIMYLWAKWSPPLLA 156
Qy 60 DFXECFVEYELKRNIGSTWTKITLNHAYKDGFDLNGKIEAKIHTLLPQCTNGSEV 119
Db 157 DASSNHLHYELRIKPEKEWETI---SVGVQTCCKINR--LNAGMRVYVQVCTLDGPE 212
Qy 120 QSSWAETTYWISPOG-IPETVQVQMDCVYNNQWYLLCSKPGIGVLLDTNLYFWYBGL 178
Db 213 WSESSERHILPQSQSPPEKPTIKRSPKEFTCWKPGDLGHPNTLYLSKEGE 272
Qy 179 DHALQCVDIYKADQNTGCRFPYLEADYKDFYICVNGSSSENKPIRSSYFTFQNLQVWP 238
Db 273 EQVYECPDY-RTAGPN-SCYFDKHTSWTITNITVTRATNEMSGSSDPHYVDVTVIYQP 330
Qy 239 LPVYVLTFTRESSCEIK---LWKS-IPLGPIPARCFDYEIR---EDDTTLTATVEN 290
Db 331 DPPVNVTELEKPKINRKYVILVTSPPPLADYRSGWLTLELRLKPEGEWETIFVQ 390
Qy 291 ET-YTLKTTNETRQLCFVVRSKVNIYCSDD--GIWSESDK 328
Db 391 QTOYKMFSLNPKKYI-----IQHCKPDHGSWSESS 425

RESULT 6
IL5R_MOUSE STANDARD; PRT; 415 AA.
AC P21183;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA CHAIN PRECURSOR (IL-5R-ALPHA).
GN IL5R OR IL5R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91092260; PubMed=2265612;
RA Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N.,
RT "Molecular cloning and expression of the murine interleukin-5
receptor."
RL EMBO J. 9:4367-4374(1990).
CC -1- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN
CC -1- BINDS TO IL-5.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

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CC -1- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO
CC ON B-CELLS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -----
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CC -----
CC EMBL: D90205; BAA14231.1; -.
CC PIR: S12357; S12357.
CC MGI: MGI:96558; IL5ra.
CC InterPro: IPR000950; -.
CC DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT DOMAIN 18 339 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 340 361 POTENTIAL.
FT DOMAIN 362 415 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 152 BY SIMILARITY.
FT DISULFID 179 193 BY SIMILARITY.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 415 AA; 46989 MW; A4326D2922571C08 CRC64;

Query Match 12.08; Score 229; DB 1; Length 415;
Best Local Similarity 24.88; Pred. No. 1e-11;
Matches 79; Conservative 56; Mismatches 135; Indels 48; Gaps 13;

Qy 34 PPQDFEIVDPVGLVYLQWQPLSLDHFKECTVEYELKRNIGSTWTKITLNHAYKD 93
Db 29 PPVNFITKATG-LAQVLLHWDNPDQEQ-RHVDLEYHVKNAPQEDYDTRKTES---KC 83
Qy 94 GFDLNGKIEAKIHTLLPQCTNGSEVQSSWAETTYWISPOGIPETKVDMDCVYNN---- 149
Db 84 VTPLHEGFAASVRLTK---SSHTTTLASSWVSAEL-KAPPGSGTSVNTLCTTHVYSS 139
Qy 150 -----WQY-LLCSWKPGIGVLLDTNLYNLFYWEGLDHALQCVDIK-ADGNTGCRFP- 200
Db 140 HTHLRPYQVSLRCTLWLVGKDAPEDTQYFLYRFGVLTE--KCQEYSRDALNRNTACWPPR 197
Qy 201 -YLEASDYKDFYICVNGSSSENKPIRSSYFTFQNLQVIVPLPVLTFTRESSCEIKLWS 259
Db 198 TFINSGEQLAVHINGSKRAAKKPFQDLSPALDQVNPRTVTVIESN-SLIQWE 256
Qy 260 IPLGPIPARCFDYEIRREDD-----TTLVATVENETITLKTNETRQLCFV 308
Db 257 KPLSAFDPCHFCNYELKIYNTKNGHIQKELJANKFISKIDVDVTSIQ-----V 305
Qy 309 RSKVNIYCSDDGIWSEWS 326
Db 306 RAAVSSPCRMFGRGWS 323

RESULT 7
PRLR_MELGA STANDARD; PRT; 831 AA.
AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROLACTIN RECEPTOR (PRL-R) (TPRLR).
GN PRLR.
OS Meleagris gallopavo (Common turkey).

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FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 830 AA; 94507 MW; 3B074E83CDF69EFF CRC64;

Query Match 11.1%; Score 210.5; DB 1; Length 830;
Best Local Similarity 24.7%; Pred. No. 7.9e-10;
Matches 86; Conservative 47; Mismatches 156; Indels 59; Gaps 14;

Qy 18 TFGCTSSDTEIKVNPQDPEIVDPGVLG-----DPQYVDVTSIVQPDAPVNLSTKTSASTYLLAKW 150
Db 97 TTYNITVNMAMEIGSNSS-----DPQYVDVTSIVQPDAPVNLSTKTSASTYLLAKW 150

Qy 54 QPPLSLDHFKECTV-EYELKRYNIGSETWKTIIYNLHYKDGFDLNGKIEAKIHTLLPWQ 112
Db 151 SPPLADVTSHVYRELRLKPEKEWETV---SVGVOYQYKVNRLQAGVYVQVQR 206

Qy 113 CTNGSEVOSSAETTYTISPOG-IPETRVQDMQCVYVNMWYLLCSWKPGIGVLLDTNYNL 171
Db 207 CVLDIGENSESSERHIHPNGESFPEKPTIICRSPEKETFTCWKPGSGGHPNTYTL 266

Qy 172 FYWYEGDLHALQVDYIKADGONTGCRFPYLEADYKDFYICVNGSSSENKPIRSYFTFFQ 231
Db 267 LYSKEGERVYECDDY-KTAGPN-SCYPDKKHTFTWYITNITVRATNEIGSNVSDPLYVD 324

Qy 232 LQNVKPLPPVYLFTRSSCEIK-----LKWS-IPLGPIPA--RCFDYEIIEIREDDTTLV 284
Db 325 VTYIVQTPPPVNVNTELEKTKVNRKPYLVLTWSPPLADVRSGWLTLDYELRLKPEEA--- 381

Qy 285 TATVENETYTLTKTNRQLCFVW----RSKNVNYCSDD--GIWSEWS 326
Db 382 -----EWEETIFVCGOOTHYKMFSLNPGKKYIVQIHCKPDHGHGNSWS 424

RESULT 9
CYRG_HUMAN STANDARD; PRT; 369 AA.
AC P31785;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C) (INTERLEUKIN-
DE 2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64) (CD132 ANTIGEN).
GN IL2RG
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92335883; PubMed=1631559;
RA Takahashi T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,
RA Munakata H., Nakamura M., Sugamura K.;
RT "Cloning of the gamma chain of the human IL-2 receptor.";
RL Science 257:379-382(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93293887; PubMed=8514792;
RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;
RT "Characterization of the human interleukin-2 receptor gamma chain
RL gene.";
RL J. Biol. Chem. 268:13601-13608(1993).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.
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RX MEDLINE=94004847; PubMed=8401490;
RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,
RA Willard H., Henthorn P.S.;
RT "The interleukin-2 receptor gamma chain maps to Xql3.1 and is mutated
RL in X-linked severe combined immunodeficiency, SCIDX1.";
Hum. Mol. Genet. 2:1099-1104(1993).
RN [4]
RP IDENTIFICATION AS A IL-4R SUBUNIT.
RX MEDLINE=94090315; PubMed=8266076;
RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
RA Arai K.-I., Sugamura K.;
RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
RL receptors for IL-2 and IL-4.";
Science 262:1874-1877(1993).
RN [5]
RP IDENTIFICATION AS A IL-4R SUBUNIT.
RX MEDLINE=94090317; PubMed=8266078;
RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,
RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
RA Leonard W.J.;
RT "Interleukin-2 receptor gamma chain: a functional component of the
RL interleukin-4 receptor.";
Science 262:1880-1883(1993).
RN [6]
RP IDENTIFICATION AS A IL-7R SUBUNIT.
RX MEDLINE=94090316; PubMed=8266077;
RA Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
RA Leonard W.J.;
RT "Interleukin-2 receptor gamma chain: a functional component of the
RL interleukin-7 receptor.";
Science 262:1877-1880(1993).
RN [7]
RP 3D-STRUCTURE MODELING OF 57-248.
RX MEDLINE=95111955; PubMed=7529123;
RA Bamorough P., Hedgecock C.J., Richards W.G.;
RT "The interleukin-2 and interleukin-4 receptors studied by molecular
RL modelling.";
Structure 2:839-851(1994).
RN [8]
RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
RX MEDLINE=94130970; PubMed=8299698;
RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
RA de Saint Basile G.;
RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
RL severe combined immunodeficiency disease result in the loss of
RL high-affinity IL-2 receptor binding.";
Eur. J. Immunol. 24:475-479(1994).
RN [9]
RP VARIANT XSCID LYS-68.
RX MEDLINE=94375038; PubMed=8088810;
RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
RA de Saint Basile G.;
RT "Detection of three nonsense mutations and one missense mutation in
RL the interleukin-2 receptor gamma chain gene in SCIDX1 that
RL differently affect the mRNA processing.";
Genomics 21:291-293(1994).
RN [10]
RP VARIANT XSCID HIS-162.
RX MEDLINE=94300093; PubMed=8027558;
RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
RT "Impairment of ligand binding and growth signaling of mutant IL-2
RL receptor gamma-chains in patients with X-linked severe combined
RL immunodeficiency.";
J. Immunol. 153:1310-1317(1994).
RN [11]
RP VARIANT XSCID ASN-39.
RX MEDLINE=95023932; PubMed=7937790;
RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
RA de Saint Basile G.;
RT "Defective human interleukin 2 receptor gamma chain in an atypical X
RL chromosome-linked severe combined immunodeficiency with peripheral T
RL cells.";
```


RT disease.";
RL Genomics 23:69-74(1994).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
CC SEVERE COMBINED IMMUNODEFICIENCY.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U04361; AAC48403.1; -
DR HSP; P31785; 11LN.
DR InterPro; IPR000950; -
DR InterPro; IPR001777; -
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 373
FT DOMAIN 23 261
FT TRANSMEM 262 283
FT DOMAIN 284 373
FT DOMAIN 151 249
FT DISULFID 62 72
FT DISULFID 102 115
FT CARBOHYD 24 24
FT CARBOHYD 71 71
FT CARBOHYD 75 75
FT CARBOHYD 84 84
FT CARBOHYD 159 159
FT CARBOHYD 164 164
FT CARBOHYD 249 249
SQ SEQUENCE 373 AA; 42516 MW; 03A0DE1FB089D8B CRC64;

Query Match 10.8%; Score 206; DB 1; Length 373;
Best Local Similarity 27.3%; Pred. No. 7e-10;
Matches 67; Conservative 42; Mismatches 100; Indels 36; Gaps 11;

Qy 115 NGSE-----VQSSWAETTYWISPGIPETKVQDMDCVYNNWQYLLCSW-----KPGI 161
Db 31 NGNEDITPDDFTATPSET---LSVSSLPLPEVQ---CFVFNVEYMNCTWNSSEPRP-- 82
Qy 162 GVLLDTNLYFWYBGL--DHALQCVDIKADGQGNIGCRFPYLEASDYKDFVCVNGSSE 219
Db 83 -----TNLTLYHWYKNSNDKRVQEGCHYLFSEVYTAGCWLQKEEHLHYETFWQLRDRPE 137
Qy 220 NKPIRSSFTTQQLNIVPLPPVYLTFTRESCEIKLKWSTPLGIPARCFDYEIEIRD 279
Db 138 --PRQSTQKLQNLQVLPWAPENLTNLNLSQESLWS---NRHLDCLEHVHVQVRS 192
Qy 280 -DTLVTATVEN-EYTLTKTNETPQLCFVVRKSKVNIYCSDDGIWSEWSKQCEGEDLS 337
Db 193 WDRSWTEQSDVHRNFSPLPSVDGQKFTYFRVRSRNPCLGSAQRWSEWSHPPIHW-GSNTS 251
Qy 338 KKTLL 342
Db 252 KENPL 256

RESULT 11
CYRG_MOUSE

ID AC
CYRG_MOUSE STANDARD; PRT; 369 AA.
P34902;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277575; PubMed=8503926;
RA Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
RT "Cloning of the mouse interleukin 2 receptor gamma chain:
RT demonstration of functional differences between the mouse and human
RT receptors.";
RL Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBA/CA;
RX MEDLINE=93391374; PubMed=8378320;
RA Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
RT IL-2R gamma chain expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93366191; PubMed=8359699;
RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
RT gamma.";
RL Gene 130:303-304(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104285; PubMed=7805729;
RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
RA Fischer A., de Saint Basile G.;
RT "The murine interleukin-2 receptor gamma chain gene: organization,
RT chromosomal localization and expression in the adult thymus.";
RL Eur. J. Immunol. 24:3014-3018(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S;
RX MEDLINE=96341745; PubMed=8750189;
RA Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
RA Dougherty G.J.;
RT "Molecular mechanisms regulating the hyaluronan binding activity of
RT the adhesion protein CD44.";
RL J. Neurooncol. 26:231-239(1995).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D13821; BAA02974.1; -
DR EMBL; U21795; AAA64279.1; -
DR EMBL; D13565; BAA02760.1; -
DR EMBL; L20048; AAA39286.1; -

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DR EMBL; S75852; AAB32904.1; -.
DR EMBL; S75844; AAB32904.1; JOINED.
DR EMBL; S75845; AAB32904.1; JOINED.
DR EMBL; S75847; AAB32904.1; JOINED.
DR EMBL; S75848; AAB32904.1; JOINED.
DR EMBL; S75849; AAB32904.1; JOINED.
DR EMBL; S75850; AAB32904.1; JOINED.
DR EMBL; S75851; AAB32904.1; JOINED.
DR EMBL; X75337; CAA53085.1; -.
DR PIR; JN0592; JN0592.
DR PIR; JN0775; JN0775.
DR HSSP; P31785; IL1N.
DR MGD; MGI:96551; IL2rg.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 369
FT DOMAIN 23 263
FT TRANSMEM 264 284
FT DOMAIN 285 369
FT DOMAIN 151 250
FT DISULFID 62 72
FT DISULFID 102 115
FT CARBOHYD 71 71
FT CARBOHYD 75 75
FT CARBOHYD 84 84
FT CARBOHYD 96 96
FT CARBOHYD 159 159
FT CARBOHYD 164 164
SQ SEQUENCE 369 AA; 42241 MW; CB2DSAB459077AC7 CRC64;

Query Match 10.4%; Score 198.5; DB 1; Length 369;
Best Local Similarity 26.5%; Pred. No. 2.9e-09;
Matches 54; Conservative 38; Mismatches 95; Indels 17; Gaps 7;

QY 136 PETKVQDMDCVYVNYWYLLCSW----KPGIGVLLDTNLYFVYEGDLHAL--OCVDYIK 189
DB 53 PTLPLPEVQCFVFNIEYMNCTWNSSEPQA-----TNLTLYRYKVSNNFTQECSHYLF 107

QY 190 ADGQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQLQNIKVPPLPPVYLTRE 249
DB 108 SKEITSGCQIQEKEDQLYQTFVQL--QDPKQPRRAVQKLNQLNLYIPRAPENLTLSNL 165

QY 250 SSECILKWSIPLGPIPARCFDYIEIRED--DTTLVTATVENE--TYTLKTTNETRQLCFV 307
DB 166 SESQLELRWK--SRHKEKRCQLYLVQVRSNRDRSNTWELIVNHEPRFSLPSVDLKRKYTR 223

QY 308 VRSKVNIYCSDDGIWSEWSKQCV 331
DB 224 VRSRYNPICGSSQWQKWSQPVHW 247

RESULT 12
CYRG_BOVIN
ID CYRG_BOVIN STANDARD; PRT; 379 AA.
AC Q95118;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN PRECURSOR (GAMMA-C)
DE (INTERLEUKIN-2 RECEPTOR COMMON GAMMA CHAIN) (IL-2R GAMMA CHAIN) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=96268473; PubMed=8672241;
RA YOO J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
gamma gene.";
RL DNA Cell Biol. 15:453-459(1996).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-----
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DR EMBL; U33748; AAB07812.1; -.
DR HSSP; P31785; IL1N.
DR InterPro; IPR000950; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002465; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 379
FT DOMAIN 23 269
FT TRANSMEM 270 290
FT DOMAIN 291 379
FT DOMAIN 158 256
FT DISULFID 109 122
FT DISULFID 68 78
FT CARBOHYD 77 77
FT CARBOHYD 81 81
FT CARBOHYD 90 90
FT CARBOHYD 166 166
FT CARBOHYD 171 171
SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 9.9%; Score 187.5; DB 1; Length 379;
Best Local Similarity 26.1%; Pred. No. 2.4e-08;
Matches 57; Conservative 41; Mismatches 93; Indels 27; Gaps 9;

QY 135 IPETKVQDMDCVYVNYWYLLCSW----KPGIGVLLDTNLYFVY----EGLDHALQCV 185
DB 61 LPLPKVQ---CFVFNIEYMNCTWNSSEPQA-----NNLTLYRYNFGDDKLECG 110

QY 186 DYKADQNGICRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQLQNIKVPPLPPVYLT 245
DB 111 HYLFSGEGITSGCFVFNIEYMNCTWNSSEPQA-----NNLTLYRYNFGDDKLECG 168

QY 246 FTRESCEILKWSIPLGPIPARCFDYIEIRED--DTTLVTATVENE--TYTLKTTNETRQ 303
DB 169 LRNLSEFQLELSWS---NRYLDHCLEHLVQVRSNRDRSNTWELIVNHEPRFSLPSVDLKR 225

QY 304 LCFVRSKVNLYCSDDGIWSEWSKQCV 341
DB 226 YTFVRSRYNPICGSAQHWSDWYPIHW--GSNTSKENI 262

RESULT 13
IL3B_MOUSE
ID IL3B_MOUSE STANDARD; PRT; 878 AA.
AC P26954;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)

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QY 191 DQONIGCREPYLEASDYKDFYICVN-----GSSENKPIRSSYFTFQLONIWKPLPPVYL 245
Db 76 SGN-SCFESKQYTSIWKIYIITVNATNMGSSSDPL-----YVDVTYIVEPEPRNLT 129
QY 246 F-----TRESSCEIKLWSIP-LGPIPARCFDYEIREDDTTLVTATVENETYTLKTTNE 300
Db 130 LEVKOLKDKTYLWVKWSPPTITDVKTGFTMEYER-----LKPEAEWEIHFTH 182
QY 301 TRQL-----CFVVRKVNIIYCSDDGINSWSDKQCWE 332
Db 183 QTQFKVEDLYPCQKYLVTQCK---PDHGYWRWSQESSVE 220

Search completed: September 1, 2001, 19:16:26
Job time: 508 sec

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OM protein - protein search, using sw model
Run on: September 1, 2001, 19:15:53 ; Search time 68.62 seconds
(without alignments)
661.332 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_343
Perfect score: 1901
Sequence: 1 MAFVCLAIGCLYFLISTTF.....EWSDKQCWGEDLSKTKTLR 343

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	1184	62.3	383	11	088786		O88786 mus musculus
2	294.5	15.5	420	4	Q14633		Q14633 homo sapien
3	293.5	15.4	396	4	Q14631		Q14631 homo sapien
4	292	15.4	333	4	Q15469		Q15469 homo sapien
5	284.5	15.0	415	11	Q9Z0K4		Q9Z0K4 cavia porce
6	260	13.7	349	6	Q97597		Q97597 bos taurus
7	241.5	12.7	279	4	Q3UDY5		Q9udy5 homo sapien
8	190.5	10.0	363	13	Q9DEQ1		Q9degl oncorhynch
9	173.5	9.1	881	13	Q57519		O57519 xenopus lae
10	167	8.8	611	13	Q9PTI0		Q9pt10 xenopus lae
11	167	8.8	622	6	Q9NB07		Q9nb16 xenopus lae
12	167	8.8	622	6	Q9NB07		Q9n0j7 callithrix
13	165	8.7	296	6	Q18880		Q18880 bos taurus
14	165	8.7	896	11	Q64146		Q64146 rattus norv
15	159.5	8.4	890	11	Q9Z1A0		Q9z1a0 cavia porce
16	159	8.4	227	6	Q9GLW3		Q9glw3 ursus marit
17	157	8.3	581	6	O46561		O46561 ovnis aries
18	156	8.2	625	6	Q9XS92		Q9xs92 trichosurus
19	154.5	8.1	611	13	Q9PTH9		Q9pth9 xenopus lae

20	151	7.9	206	4	Q16354		Q16354 homo sapien
21	151	7.9	349	4	Q9UJH5		Q9uhj5 homo sapien
22	147.5	7.8	538	13	Q9DFU0		Q9dfu0 sparus aura
23	146.5	7.7	422	4	Q9UHH5		Q9uhh5 homo sapien
24	145.5	7.7	217	6	Q46386		O46386 mustela vis
25	145.5	7.7	422	4	O75462		O75462 homo sapien
26	143.5	7.5	425	11	Q9JM58		Q9jms8 mus musculus
27	143.5	7.5	918	13	Q9W609		Q9w6u9 gallus gall
28	132	6.9	346	13	Q93404		O93404 oreochromis
29	130.5	6.9	198	6	O18985		O18985 cervus elap
30	130.5	6.9	390	4	Q9UEH7		Q9ueh7 homo sapien
31	126.5	6.7	329	4	Q9UQ41		Q9uq41 homo sapien
32	117.5	6.2	896	4	Q13594		Q13594 homo sapien
33	117.5	6.2	906	4	Q13593		Q13593 homo sapien
34	117.5	6.2	958	4	Q13592		Q13592 homo sapien
35	116.5	6.1	1282	5	Q9WEO0		Q9wEO0 drosophila
36	114	6.0	371	4	Q9HC73		Q9hc73 homo sapien
37	114	6.0	894	6	Q9MYL1		Q9myl1 macaca mula
38	114	6.0	925	6	Q9MYK9		Q9myk9 macaca mula
39	114	6.0	1163	6	Q9MYL2		Q9myl2 macaca mula
40	113	6.0	1194	6	Q9MYL0		Q9myl0 macaca mula
41	113.5	6.0	896	4	Q9Z919		Q9z919 homo sapien
42	113.5	6.0	958	4	Q9Z920		Q9z920 homo sapien
43	113.5	6.0	1165	4	Q9Z921		Q9z921 homo sapien
44	109.5	5.8	26926	4	Q10466		Q10466 homo sapien
45	109	5.7	2221	5	Q9U1M1		Q9u1m1 drosophila

ALIGNMENTS

RESULT 1
O88786 PRELIMINARY; PRT; 383 AA.
AC O88786;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IL-13 RECEPTOR ALPHA 2.
GN IL13RA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ; TISSUE=THYMUS;
RX MEDLINE=98391042; PubMed=9725226;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,
RA Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,
RA Collins M.;
RT "The murine IL-13 receptor alpha 2: molecular cloning,
RT characterization, and comparison with murine IL-13 receptor alpha 1.";
RL J. Immunol. 161:2317-2324(1998).
DR EMBL; U65747; AAC33240.1; -
DR MGD; MGI:1277954; IL13ra2.
DR InterPro; IPR002596; -
DR InterPro; IPR003532; -
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;

Query Match 62.3%; Score 1184; DB 11; Length 383;
Best Local Similarity 64.0%; Pred. No. 1.1e-99;
Matches 213; Conservative 46; Mismatches 68; Indels 6; Gaps 2;
QY 1 MAFVCLAIGCLYFLISTTFGCTSSSDTEIKVNPQDFIVDPGYLYLQWPPPLSD 60
Db 1 MAFV-HRCLCFLICITIGYS----LEIKVNPQDFEILDGLGYLYLQWPPVIE 54
QY 61 HFPECTVEYELKYNIGSETWTKTITIKNLHYKDGFDLKNKGIEAKIHTLPLWCTNGSEVQ 120
Db 55 KFKGCTLEYELAYNRVSDSWKTIITRNLIYKDGFDLKNKGIEGKIRTHLSEHTNGSEVQ 114

[illegible]

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QY 53 WOPPLSLDFHFKECTVEYELKYNIGSETWKTITIKNLHYKDFDLNKGIEAKIHTLLPWQ 112
DB 18 WNPPEGAS--PNCSLKY---FSHFGKQDKKIAPET-HRSKEVPLNERICLQVGS---Q 67
QY 113 C-TNGSEVQSSWAETTYWISQGPETKVDQMDCVYVWQYLLCSWKPGIGVLLDTNVL 171
DB 68 CSTNESEKPSILVEKCF-SPPEGDPESAVALQCIWHNLRYMKCTWLPGRNASPDPNIL 126
QY 172 FYWYEGDLHALQCVDYIKADGNICRPPYLEASD--YKDFYICVNGSSSENKPIRSSYET 229
DB 127 YWHSNLSGKIQCENFYR-EGQHACSFLNLYKVDSSFEQHSQVQWVRDNAGKISPSFNI 185
QY 230 FOLQNVKPLPPVYLTFRESCEIKLWSIPLGPIPARCFDYEIEIREDDTTTLVTATVE 289
DB 186 VFLTSHVRP-DPSHIKLSFQNGDLVQWTPQN-FQSQCLCYEVEVINSHA----- 235
QY 290 NETYTLTKTNTETR-----QLCFVY-----RSKNVIYC-SDDGIWS 323
DB 236 -ETHDIFYVEAKQNTFEGNLEGTCFVMPVGLPDLTNTVRIRVKTNKLCEDDKLWS 294
QY 324 EWS 326
DB 295 NWS 297
RESULT 7
Q9UDY5 PRELIMINARY; PRT; 279 AA.
AC Q9UDY5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81380; ADO0511.2; -
DR HSSP; P40189; 1BQU.
DR InterPro; IPR002996; -
DR InterPro; IPR003532; -
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 279 AA; 31658 MW; E74141FE9F8E9EBB CRC64;
```

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Query Match 12.7%; Score 241.5; DB 4; Length 279;
Best Local Similarity 27.7%; Pred. No. 4e-14;
Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;
QY 11 LYTFLLSTFTGCTSSDTEIKVNPQDPEIYDPGYLYLQWQPPSLDHFKECTVEY- 69
DB 10 LWALLLCAGGGGGGGAAPTETQPPVTNLSVSNELCTVITWNPPEGAS--SNCSLWYF 67
QY 70 ---ELKVRNIGSETWKTITIKNLHYKDFDLNKGIEAKIHTLLPWQ--TNGSEVQSSWA 124
DB 68 SHFGKQDKKIAPETRRSI-----EVLNERICLQVGS---QCSTNESEKPSILV 114
QY 125 ETTYWIS--PQGPETKVDQMDCVYVWQYLLCSWKPGIGVLLDTNLYFWYEGDLHALQ 183
DB 115 EKC--ISPEGDPESAVALQCIWHNLRYMKCTWLPGRNASPDPNILYWHRSLEKIHQ 172
QY 184 CVDYIKADGNICRPPYLEASD--YKDFYICVNGSSSENKPIRSSYFTFQIQNVKPLPP 241
DB 173 C-ENIFREGQVFGGCSFDLTVKDSSFEQHSQIMVKDNAGKIKPSFNIVPLTSRVKPDPP 231
QY 242 --VYLTFRESCEIKLWSIPLGPIPARCFDYEIEIREDDT 281
DB 232 HIKNLSFHND---DLYVQWENPQNF1-SRCLFYEVEVNNSTQ 269
```

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RESULT 8
Q9DEQ1 PRELIMINARY; PRT; 363 AA.
AC Q9DEQ1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang T., Secombes C.J.;
RT *Cloning and expression of the first non-mammalian cytokine receptor
RT common gamma chain gene in rainbow trout (Oncorhynchus mykiss).;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276623; CAC09429.1; -
KW Receptor.
FT NON_TER
SQ SEQUENCE 363 AA; 41861 MW; DF69B2EB3EEA06D3 CRC64;
Query Match 10.0%; Score 190.5; DB 13; Length 363;
Best Local Similarity 22.9%; Pred. No. 2.4e-09;
Matches 55; Conservative 48; Mismatches 118; Indels 19; Gaps 6;
QY 97 LNKIEAKIHTLLPWQCTNGSEVQSSWAETTYWISQGPETKVDQMDCVYVWQYLLCS 156
DB 1 IHKYVRVELYTLIPTVTHFDKMKVGSW--LFLLSLQGYEAPSTPNVNCILINDYVNCI 58
QY 157 WKPGIGVLLDTNLYFWYEGDLHALQCVYIKADGNICRPPYLEASDYKDFYICVNG 216
DB 59 WSE--QSIPEVNFTEFSRFRFKDNMECTYLOEASVAVGCRSLYDKSRDRF----- 108
QY 217 SSENKPIRSSYFTFQ---LQNVKPLPPVYLTFRESCEIKLWSIPLGPIPARCFDYE 273
DB 109 TLTKLVHQNMSYVDHNLKSVKLYDPPVNLVSVMKNKDPNLNLYNNKNTF---CIESE 165
QY 274 IEIREDDTTLVTATVENE--TYTLTKTNTETROLCFVRSKVNICYSDGIGSEWSQKQWE 332
DB 166 VRYRNSDKWKTSTPSKEQKAVAFPLKSSRYEQVRAVRVNDMCGESEFSEWSQPTOWD 225
RESULT 9
O57519 PRELIMINARY; PRT; 881 AA.
AC O57519
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GPL30P1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC03531.1; -
DR HSSP; P40189; 1BQU.
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003529; -
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
```

DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match 9.1%; Score 173.5; DB 13; Length 881;
Best Local Similarity 25.0%; Pred. No. 2.6e-07;
Matches 75; Conservative 37; Mismatches 115; Indels 73; Gaps 14;

QY 68 EYELKYNIGSTWTKTIITKLNHYKDGFLNKGIEAKIHTLLPWQCTNGSEVQSSWAET 127

DB 74 QYEILNQTTSSVTFFENLTILN-----SPLTCNVASGHV-----ANTL 111

QY 128 YWISQGIPTKQVDMDCVYNNWQYLLCSWRKPGIGVLDNTNLFY-W-YEGLDHALQC 184

DB 112 YGIFFTLGLPPDKPTNLCTCIVVQNQDLNLTCTWDPRTNLPTNYTLSHRWAGANY---- 167

QY 185 VDIKADQNGICRPPYLEASDYKDFYICVNGSSSENKPIRSSYFTFQLONIYKPLPPYV- 243

DB 168 -----CGANNSTHTSPGQFYIDTTFQVEATNELGIQKSETLTIDPYNIVKPNPPQLS 222

QY 244 -LTFYRESSCEIKLWSIPLGPI-----PARCFDYEIEIREDDTTLVTATVENET 292

DB 223 ELISLELPAALKIEKNPITAFNLKYNIRPVKTQDWEM-VEEDI-----ASHRDS 276

QY 293 YTLK-----TTNETROLCFVVRSKVNIYCSDDGIWSEWSD--KQCW-----EGEDLSKK 339

DB 277 FTQLDLLPNTVVEVSIRC-----IHKDGHGFWSDWSELKQVTPPEAPPSRGPDINKK 328

RESULT 10

ID Q9PTIO PRELIMINARY; PRT; 611 AA.

AC Q9PTIO;

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DE PROLACTIN RECEPTOR A.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8335;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20087225; PubMed=10618394;

RA Huang H., Brown D.D.

RT "Prolactin is not a juvenile hormone in Xenopus laevis

metamorphosis.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).

DR EMBL; AF193800; AAF05776.1; -.

DR HSSP; P16471; 1BP3.

DR InterPro; IPR001777; -.

DR InterPro; IPR002996; -.

DR Pfam; PF00041; fn3; 1.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.

DR SMART; SM00060; FN3; 1.

KW Receptor.

SQ SEQUENCE. 611 AA; 68255 MW; 85629F917766FFB6 CRC64;

Query Match 8.8%; Score 167; DB 13; Length 611;

Best Local Similarity 27.6%; Pred. No. 6.4e-07;

Matches 64; Conservative 30; Mismatches 100; Indels 38; Gaps 10;

QY 127 TYWISQGIPTKQVDMDCVYNNWQYLLCSWRKPGIGVLDNTNLFYWYEGLDHALQCVD 186

DB 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPFGSDGGLPTNYSLLYRKENDPKIYECPD 80

QY 187 YIKADQNGICRPPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFQLONIYKPL 239

DB 81 YV-TSGLN-SCFFDKAHTSFWIFYHYVNNATLGSNVSDEESVDITY-----IVQPY 131

QY 240 PPVYLTFYRESS-CEIKLWSIPLGPIPARCFD-----YEIEIRDDTTLVTATVE 289

DB 132 PPTNVSLAVESGHHDLLK-----LPPAMVDVQSGWLTLLAYEVRYKEKEQWEAHLV 185

QY 290 NETYILKTTNETROLCFVVRSKVNIYCS-DDGIWSEWSDKQWEGEDLSKKT 340

DB 186 GNQLKLLKFLGTPGGNYVVO-----VRCKPDSGHWSEWSTESYIQIPGGGKKT 233

RESULT 11

Q9IBF6

ID Q9IBF6 PRELIMINARY; PRT; 611 AA.

AC Q9IBF6;

DT 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

DE PROLACTIN RECEPTOR.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8335;

RN [1]

RP SEQUENCE FROM N.A.

RA Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;

RT "Cloning of a cDNA for Xenopus prolactin receptor and its

metamorphophic expression profile.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB030443; BAA90400.1; -.

DR InterPro; IPR001777; -.

DR InterPro; IPR003528; -.

DR Pfam; PF00041; fn3; 1.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.

DR SMART; SM00060; FN3; 1.

KW Receptor.

SQ SEQUENCE. 611 AA; 68315 MW; 7E0DF76F21D8CE97 CRC64;

Query Match 8.8%; Score 167; DB 13; Length 611;

Best Local Similarity 27.6%; Pred. No. 6.4e-07;

Matches 64; Conservative 30; Mismatches 100; Indels 38; Gaps 10;

QY 127 TYWISQGIPTKQVDMDCVYNNWQYLLCSWRKPGIGVLDNTNLFYWYEGLDHALQCVD 186

DB 22 TVSLNAQSLPGKPVID-KCRSYEKVTFSCWKPFGSDGGLPTNYSLLYRKENDPKIYECPD 80

QY 187 YIKADQNGICRPPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFQLONIYKPL 239

DB 81 YV-TSGLN-SCFFDKAHTSFWIFYHYVNNATLGSNVSDEESVDITY-----IVQPY 131

QY 240 PPVYLTFYRESS-CEIKLWSIPLGPIPARCFD-----YEIEIRDDTTLVTATVE 289

DB 132 PPTNVSLAVESGHHDLLK-----LPPAMVDVQSGWLTLLAYEVRYKEKEQWEAHLV 185

QY 290 NETYILKTTNETROLCFVVRSKVNIYCS-DDGIWSEWSDKQWEGEDLSKKT 340

DB 186 GNQLKLLKFLGTPGGNYVVO-----VRCKPDSGHWSEWSTESYIQIPGGGKKT 233

RESULT 12

Q9NOJ7

ID Q9NOJ7 PRELIMINARY; PRT; 622 AA.

AC Q9NOJ7;

DT 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)

DE PROLACTIN RECEPTOR PRECURSOR.

OS Callithrix jacchus (Common marmoset).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.

OX NCBI_TaxID=9483;

RN [1]

RP SEQUENCE FROM N.A.
RA Dairyple A., Edery M., Jabbour H.;
RT "Sequence and functional characterisation of the marmoset monkey
RT (Callithrix jacchus) prolactin receptor: comparative homology with the
human long form prolactin receptor."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ272217; CAB75847.1; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal; Receptor.
FT CHAIN 1 24 POTENTIAL.
FT CHAIN 25 622 PROLACTIN RECEPTOR.
SQ SEQUENCE 622 AA; 69425 MW; 65F99522C6D6DB6 CRC64;

Query Match 8.8%; Score 167; DB 6; Length 622;
Best Local Similarity 28.8%; Pred. No. 6.6e-07;
Matches 61; Conservative 26; Mismatches 91; Indels 34; Gaps 10;

QY 131 SPQGPETKQVDMDCVYVNWQYLLCSWKPGIGVLLDTNLYFWYEGDLHALQCVDYKKA 190
DB 26 SPFGKPEI-----FKCRSPNKETTCWRPGADGGLPTNYSLAYHREGEKFIHECPDYV-T 80
QY 191 DQONTGCRPPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNVKPLPPVYLFTRES 250
DB 81 GGNP-SCHGKQYTSWRYIITVATNEMGSLDSEIYVDVYIVEDPPUNVY----- 134
QY 251 SCEIK-----LKWSIP-LGPIPARCFD--YEIEIREDDTLVLTATVENETYLTKT 297
DB 135 -VEVQPEDKPKYLWIKWSPPLDLKLTGWFTLLYEQIKPENAE-----EMETHFAQ 187
QY 298 TNETQLCFVRSK--VNIYCS-DGIGSEWS 326
DB 188 QTDKVLSLHPGQKYLQVVRCKPDHGYWSSWS 219

RESULT 13
O18880
ID O18880 PRELIMINARY; PRT; 296 AA.
AC O18880;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR SHORT FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97375450; PubMed=9231767;
RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
RT tissues."
RL Endocrinology 138:3187-3194(1997).
DR EMBL; AF027403; AAB83999.1; -
DR HSP; P14787; IAN3.
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003528; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 296 AA; 33854 MW; 9F1C15FB41DE0787 CRC64;

Query Match 8.7%; Score 165; DB 6; Length 296;
Best Local Similarity 31.3%; Pred. No. 4e-07;

Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;
QY 136 PETKQVDMDCVYVNWQYLLCSWKPGIGVLLDTNLYFWYEGDLHALQCVDYKKA 195
DB 27 PPEKPLVKCRSPGKETTCWRPGADGGLPTNLYTHKEGETLIHECPDY-KTGGPN- 84
QY 196 GCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTFOLQNVKPLPPVYLFTRES 255
DB 85 SCYFSKHTSIWKWYITVNAIQMGISSDPLYYVHVYVIVEPEPPANLTLELKHPRK 144
QY 256 ---LKWSIP-LGPIPARCFD--YEIEIREDDTLVLTATVENET-YLTKTN-ET 306
DB 145 PYLWIKWSPPTMTDVKSGWFIQYIRLKPENAE-----DMETHFTLKQTLKIFN 198
QY 307 VVRKVNLYCS-DGIGSEWS 326
DB 199 GQYLVQIRCPDHGYWSEWS 219

RESULT 14
O64146
ID O64146 PRELIMINARY; PRT; 896 AA.
AC O64146;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
GN RIL-3R<BETA>
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370942; PubMed=7643220;
RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
RT microglia and its mRNA expression in vivo."
RL J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RA Gebicke-Haerter P.J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; S79263; AAB35068.1; -
DR EMBL; AJ000555; CAA04186.1; -
DR InterPro; IPR000282; -
DR InterPro; IPR001777; -
DR InterPro; IPR002996; -
DR InterPro; IPR003531; -
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal.
FT NON_TER 1 1
FT NON_TER 896 896
SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

Query Match 8.7%; Score 165; DB 11; Length 896;
Best Local Similarity 20.5%; Pred. No. 1.6e-06;
Matches 77; Conservative 62; Mismatches 156; Indels 80; Gaps 18;

QY 5 CLATGCL--YT-FLISTTFGCTSSSDYEIKVN-----PPQFEIVDVGYLGL 49
DB 94 CVPRRCVLPYTFQFSVKEDYISLQDRDLSIHLVPLAQHVQPPPKDISISPSG--DHF 151
QY 50 YLQWQPPPL---SLDHFKECTVEYELKYNIGSETWKTITIKNLHYKDFDLNKGTEAKIH 106
DB 152 LLKWSVPLGDAQVSLLSQKDIQFVAYKQL-QDSWED--ASSLH-----TCNLWLTPEK 203
QY 107 TLLP-----WQCTNGSEVQ---SSWAETTWISQIPETKQVDMDCVYVNWQYLL 154

204	Db	LFLPNSIYVARVRAQLAPAGSSLSGRGSHSPVHWDSPTE-DKARPQNLCQFFDGIQSLN	262
155	QY	CSWKPGIGVLLDNYNLYFWYEGDLHALQCVDIKADGONIGREFPYLEASDYKDFYICV	214
263	Db	CSNEVMTKVTDVSFGLFYSSSPKACEKCCSPWKE-----LQASRYTRYHCSL	311
215	QY	NGSSENKPIRSSYFTFQLQ-----NIVKPLPP-VYLTFTRESSECKLKWISPL	262
312	Db	NVSD---PAAHSQYTSVVRKLEOGKFIESFNHQMNPPTLINTKNRDS---YSLHWETQK	365
263	QY	GP1PARCFDEYIEIR-----EDDTPLVATVENETNYTLTKTNETQLCFVVRKSNIVYC	316
366	Db	MSYPFTQHAFOVQYKKKLDREWEDSKT-----ENLNHAHSMDLQLEPGTSYCARVRVKTIP	421
317	QY	SDDGIWSEWSDKOCW	331
422	Db	EYKGLWSEWSNECTW	436

RESULT 15

Q921A0	PRELIMINARY;	PRT;	890 AA.
ID	Q921A0		
AC	Q921A0;		
DT	01-MAY-1999 (trEMBLrel. 10, Created)		
DT	01-MAY-1999 (trEMBLrel. 10, Last sequence update)		
DT	01-MAR-2001 (trEMBLrel. 16, Last annotation update)		
DE	INTERLEUKIN-5 RECEPTOR BETA CHAIN.		
GN	IL5.		
OS	Cavia porcellus (Guinea pig).		
OC	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.		
OX	NCBI_Taxid=10141;		
RN	[1]		
RA	SEQUENCE FROM N.A.		
RP	Legsdon N.J., Graham A., Scott C.W.;		
RT	"Guinea pig IL5 receptor beta chain.";		
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; U94688; AAC7520.1; -;		
DR	InterPro; IPR000276; -;		
DR	InterPro; IPR001777; -;		
DR	InterPro; IPR002996; -;		
DR	InterPro; IPR003531; -;		
DR	Pfam; PF00041; fn3; 3.		
DR	PROSITE; PS00237; G.PROTEIN_RECPT; UNKNOWN_1.		
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.		
DR	SMART; SM00060; FN3; 1.		
DR	Receptor.		
Q921A0	SEQUENCE	890 AA;	96578 MW; D43FB1CA88525536 CRC64;

[illegible]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:07:53 ; Search time 43.66 Seconds
(without alignments)
649.036 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_372

Perfect score: 2056

Sequence: 1 MAFVCLAIGCLYFLISTTF.....ILVIFVTGLLLRKPNTPKMK 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	310.5	15.1	420	2 S21052	interleukin-5 rece
2	292	14.2	335	2 A40267	interleukin-5 rece
3	261	12.7	831	2 JQ1655	prolactin receptor
4	241	11.7	415	2 S12357	interleukin-5 rece
5	220	10.7	369	2 A42565	interleukin-2 rece
6	216.5	10.5	830	2 I50455	prolactin receptor
7	212.5	10.3	369	2 I49280	interleukin-2 rece
8	208	10.1	373	2 A55718	interleukin-2 rece
9	195	9.5	878	1 A40091	interleukin-3 rece
10	180.5	8.8	897	1 A39255	cytokine receptor
11	178	8.7	896	2 I56563	interleukin-3 rece
12	173.5	8.4	896	1 A35782	cytokine receptor
13	165	8.0	310	2 A29884	prolactin receptor
14	165	8.0	412	2 A41070	prolactin receptor
15	165	8.0	581	2 I45971	prolactin receptor
16	165	8.0	610	2 A34631	lactogen receptor
17	165	8.0	610	2 A36116	prolactin receptor
18	159	7.7	292	2 I77525	prolactin receptor
19	159	7.7	303	2 I77524	prolactin receptor
20	159	7.7	608	2 I53269	prolactin receptor
21	151	7.3	622	2 A40144	prolactin receptor
22	150.5	7.3	917	2 I49699	glycoprotein 130 -
23	149	7.2	616	2 A30304	prolactin receptor
24	142.5	6.9	400	2 S06945	granulocyte-macrop
25	138	6.7	378	2 A40266	interleukin-3 rece
26	134.5	6.5	1097	2 S17308	leukemia inhibitor
27	133.5	6.5	333	2 S13684	granulocyte-macrop
28	133.5	6.5	378	2 S50040	granulocyte-macrop
29	131.5	6.4	630	2 I51086	prolactin receptor

ALIGNMENTS

RESULT 1

S21052

interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C:Accession: S21052; S21050; S21053; A46175; S78107
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tominaga, A.; Takatsu, K.
J. Exp. Med. 175, 341-351, 1992
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.
A:Reference number: S21050; MUID:92121815
A:Accession: S21052

A:Residues: 1-420 <MUR>

A:Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844
A:Experimental source: clone lambda h5R.12

A:Accession: S21050

A:Molecule type: DNA

A:Residues: 1-395, 'I' <MU2>

A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840
A:Experimental source: clone lambda h5R.27

A:Accession: S21053

A:Molecule type: mRNA

A:Residues: 1-332, 'K' <MU3>

A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466
A:Experimental source: clone lambda h5R.25

R:Ravennier, J.; Tuppens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devos, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992
A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum

A:Reference number: A46175; MUID:92357767

A:Accession: A46175

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 333-420 <TAV>

A:Experimental source: HL-60 cells and eosinophils

A:Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244)
R:Murata, Y.

submitted to the EMBL Data Library, July 1991

A:Reference number: S78106

A:Accession: S78106

A:Molecule type: DNA

A:Residues: 1-128, 'I' <MUW>

A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840

R:Murata, Y.

submitted to the EMBL Data Library, September 1991

A:Reference number: S78107

A:Accession: S78107

A:Molecule type: mRNA

A:Residues: 1-128, 'I' <MU4>

A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466

C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-420/Product: interleukin-5 receptor alpha chain #status predicted <NAT>

F:345-365/Domain: transmembrane #status predicted <TMM>
F:35,131,137,142,216,244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.1%; Score 310.5; DB 2; Length 420;
Best Local Similarity 27.9%; Pred. No. 3.4e-17;
Matches 99; Conservative 64; Mismatches 151; Indels 41; Gaps 15;

```
QY 27 DTEIKVNPQDPEIVDPGVLGYLYLQWPPSLDHFKECTVEYELKYRIGSETWKTIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLLPVPNTIKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPREDDET 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKDGFDLANKGEAKIHTLLPQCTNGSEVQSWAETTWISPOGIPETKVQDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSAVRTILQ---NDHSLASSWASAEHL-APPGSPGTSVNLCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YNNQYLL-CSWKPGIGVLLDFTNLYFY----WYEGLDHALQCVDIKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TWTEDNYSRLRSYQVSLHCTVLGTDAPEDTQYFLYRYGSWTE-----ECQESKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -QONICCRFP--YLASDYKDFYICVNGSENKPIRSSYFTFQLNIVKPLPPVLTFR 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACFPFRFILSKGRDNLAVLVNGSSKHSARPPDQFALHAIDQINPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVATVENETVTLKTTNETROLCFV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 EGT-RLSIQWKPVSAPFPHCFDYEYVKIHNRNGYLQIEKLTNAFISIIDLSKYDVQV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 309 RSKVNIYSDGDIWSESKQWEGEDLSKTLRLFWLPGFILLIVFTVGLLL 363
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 RAAVSSMCREAGLWSEWS-OPIYVGNDEHKP--LREW----FVIVIMATICFILL 356
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 2

A40267
Interleukin-5 receptor alpha chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C:Accession: A40267
R:Tavernier, J.; Devos, R.; Cornelis, S.; Tulpens, T.; Van der Heyden, J.; Fiers, W.; Pl
Cell 66, 1175-1184, 1991
A:Title: A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-speci
A:Reference number: A40267; MUID:92005669
A:Accession: A40267
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-335 <TAV>
A:Cross-references: GB:M75914; NID:g186387; PIDN:AAA36110.1; PID:g186388
C:Keywords: cytokine receptor; transmembrane protein

Query Match 14.2%; Score 292; DB 2; Length 335;
Best Local Similarity 28.0%; Pred. No. 7.5e-16;
Matches 89; Conservative 56; Mismatches 139; Indels 34; Gaps 12;

```
QY 27 DTEIKVNPQDPEIVDPGVLGYLYLQWPPSLDHFKECTVEYELKYRIGSETWKTIT 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 DEKISLLPVPNTIKVTG-LAQVLLQWKNPDQEQ-RNVNLEYQVKINAPREDDET 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 KNLHYKDGFDLANKGEAKIHTLLPQCTNGSEVQSWAETTWISPOGIPETKVQDMDCV 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 ES---KCVTILHKGFSAVRTILQ---NDHSLASSWASAEHL-APPGSPGTSVNLCT 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 -----YNNQYLL-CSWKPGIGVLLDFTNLYFY----WYEGLDHALQCVDIKAD 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 TWTEDNYSRLRSYQVSLHCTVLGTDAPEDTQYFLYRYGSWTE-----ECQESKDT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 -QONICCRFP--YLASDYKDFYICVNGSENKPIRSSYFTFQLNIVKPLPPVLTFR 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 LGRNIACFPFRFILSKGRDNLAVLVNGSSKHSARPPDQFALHAIDQINPLNVTAEI 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 249 ESSCEIKLWSIPLGPIPARCFDYEIEIREDDTTLVATVENETVTLKTTNETROLCFV 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Db 250 EGT-RLSIQWKPVSAPFPHCFDYEYVKIHNRNGYLQIEKLTNAFISIIDLSKYDVQV 308
QY 309 RSKVNIYSDGDIWSEWS 326
 :
Db 309 RAAVSSMCREAGLWSEWS 326
 :
RESULT 3
JQ1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: JQ1655; MUID:93075121
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A:Experimental source: kidney
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRSI>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TMM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

Query Match 12.7%; Score 261; DB 2; Length 831;
Best Local Similarity 26.3%; Pred. No. 7e-13;
Matches 98; Conservative 55; Mismatches 175; Indels 44; Gaps 16;

```
QY 18 TTFGCTSSDTEIKVN--PPQDFE---IVDPQ-----YLGVLVLOWOPPLSL 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 97 TTFNITVATNEIGNSSDPQVVDVTSIVQSPVNLITETRSANIMYLWAKWSPPLLA 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 DHFKECTVEYELKYRIGSETWKTITNLNHYKDGFDLANKGEAKIHTLLPQCTNGSEV 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 157 DASSNHLHYELRIKPEKEEWETI---SVGVTQCKINR-LNAGMRVYVQVRCITDPE 212
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 QSSWAETTWISPOG-IPETKVQDMDCVYNNQYLLCSWKPGIGVLLDFTNLYFYWYEG 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 WSEWSEERHILIPQSGSPPEKPTIICRSPEKETTCWKKPGLDGGHPNTYLLYSKEGE 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 DHALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFQLNIVKP 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 273 EQVYECPDY-RTAGPN-SCYFDKHTSFTYIYIIVRATNEMSGNSSDPHYVDVYIVQP 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 239 LPVYLVTTRSSCEIK-----LKWS-IPGPIPARCFDYEIEIR---EDDTTLVATVEN 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 331 DPPVNVTLLELAKPKINRKPVLVLTWSPPPLADVRSGLWLTLEYELRLKPEGEWETIFVQ 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 ET-YTLKTTNETROLCFVVRKSNVLYCSDD--GISEWSDKOCWE-GEDLSKTKILLRWL 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 391 QTYQKMFSLNPGKKYI-----IQHCKPDHHSWSESSSENYIQIPNDFVRKDMI-VMI 443
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 347 PFGFILLIVFV 358
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 444 VLGVLSSLICLI 455
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 4

Sl2357
interleukin-5 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: Sl2357
R:Takaki, S.; Tominaga, A.; Hitoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu
EMBO J. 9, 4367-4374, 1990

A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.
A:Reference number: S12357; MUID:91092260
A:Accession: S12357
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-415 <TAK>
A:Cross-references: GB:D90205; NID:g220465; PIDN:BAAL4231.1; PID:g220466
C:Keywords: cytokine receptor; transmembrane protein

Query Match 11.7%; Score 241; DB 2; Length 415;
Best Local Similarity 24.9%; Pred. No. 1.1e-11;
Matches 88; Conservative 65; Mismatches 144; Indels 56; Gaps 17;
Qy 34 PQDPEIIVDPGVLYLQWOPPLSLDFHFKCTVEYELKYNIGSETWTKITIKNLHYKD 93
Db 29 PPNVTIKATG-LAQVLLHWDNPDEQ-RHVDLEHYHKINAPQDEVDTRKTES---KC 83
Qy 94 GFDLNGIEAKIHTLLPQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDCVYYN---- 149
Db 84 VTPLEHGEFAASVRTILK---SSHTTLASSWVSAEL-KAPPGSPGTSVNTLCTTHTTVVSS 139
Qy 150 -----WQY-LLCSNKPGLVLLDNYNLFYWEGLDHALQCVDIK-ADGONICRPP- 200
Db 140 HTHLRPYQVSLRCTLWLGKADAPEDTYFLYRFGVLTE--KCQEYSRDALNENTACWEP 197
Qy 201 -YLEASDYKDFYICVNGSENKPIRSSYFTFQLOINIVKPLPPVYLTFTRRESSCEIKLWKS 259
Db 198 TFINSKGFEQLAHVINGSKRAIRPFOLFPLAIDQVNPNNVVEIESN-SLYIQWE 256
Qy 260 IPLGPIPARCFDYEIEIRDD-----TTLVATVENETVTLTKTNETROLCFV 308
Db 257 KPLSAPPDHCNFYELKIYNTKNGHIQKEKLIANKFISKIDOVSTYSIQ-----V 305
Qy 309 RSKVNIYSDGINSWSDKQCEGDSKTLRLFW-----LPGFIIILVIF 357
Db 306 RAAVSPCRMPGRWGWS-OPIYVGKE--RKSLVE-WHLIVLPTAACFVLLIF 354

RESULT 5

A42565
Interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A42565; A46591; I54332
R:Takehita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.; Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; MUID:92335883
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TAK>
A:Cross-references: GB:D11086; NID:g303611; PIDN:BAAO1857.1; PID:g219890
A:Experimental source: MOLT beta lymphoid cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109167)
R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J. J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; MUID:93293887
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked
A:Reference number: I54332; MUID:94004847
A:Accession: I54332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>

A:Cross-references: GB:L19546; NID:g349631; PIDN:AAAC37524.1; PID:g349632
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1; IMD4
A:Cross-references: GDB:I34807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A:Note: defects are associated with an X-linked form of severe combined immunodeficiency
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

Query Match 10.7%; Score 220; DB 2; Length 369;
Best Local Similarity 25.5%; Pred. No. 4.6e-10;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;
Qy 97 LNKGIEAKIHTLLPQCTNGSE-VQSSWAETTYWISPOGIPETKVQDMDCVYNNQYLLC 155
Db 19 LGVGLNTILT-----PNGNEDTTADFLLTTPMPTDSLSVSTLPLPEVOCFVFNVMNC 72
Qy 156 SW-----KPGIGVLLDNYNLFYWEGLDH--ALQCVDIKADQNIGCRPPYLEASDY 207
Db 73 TWNSSEFQP-----TNLTLYHWYKNSDNDKVQKCHYLFESEITSCQLOKKEIHL 125
Qy 208 KDFYICVNGSENKPIRSSYFTFQLOINIVKPLPPVYLTFTRRESSCEIKLWKSIPGLPIA 267
Db 126 QTFVYVOLQDPRE--PRQATQMLKQLNVLIPWAPENLTLHLKLSQLELNWN---NRELN 180
Qy 268 RCFDYEIEIRDD-DTTLVTATVE-NETVTLTKTNETROLCFVVRKVNLYCDDGIWSEW 325
Db 181 HCLEHLVQYRTDWDHSWTEQSDYRHKFSLPSVDQCKRYTFRVRSFRNPLCQSAQHWSEW 240
Qy 326 SDKQCEGDSKTLRLFWLPGFIIILVIFVTG 360
Db 241 SHPIHW-GSNTSKEN-----PFLFALEAVVISVG 268

RESULT 6

150455
Prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C:Accession: I50455
R:Chen, X.; Horseman, N.D. Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor
A:Reference number: I50455; MUID:94283267
A:Accession: I50455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CHE>
A:Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382
C:Superfamily: cytokine receptor homology
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 10.5%; Score 216.5; DB 2; Length 830;
Best Local Similarity 24.4%; Pred. No. 2.4e-09;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;

Qy 18 TTFGCTSSSDTEIKVNPQDFEIVDPGVILG-----YLYLQW 53
Db 97 TTYNTVMMNIEIGNSS-----DPQYVDVTSIVQDAPVNLSTKTSTASTYLLAKW 150
Qy 54 QPPLSLDHFKECTV-EYELKYNIGSETWTKITIKNLHYKDGFDLNGKIEAKIHTLLPWQ 112
Db 151 SPPLADVTNSHVYRYELRLKPEKEWETV---SVGVQYQYKYNR-LQAGVKYVQVR 206
Qy 113 CTNGSEVQSSWAETTYWISPOG-IPETKVQDMDCVYNNQYLLCSWKPGIGVLLDTNVL 171
Db 207 CVLDIGSEWSERSHIHPNGESPPEPTIHKRSPEKETFTCWKPGSGGHPNTYTL 266
Qy 172 FWYEGLDHALQCVDIKADQNIGCRPPYLEASDYKDFYICVNGSENKPIRSSYFTFQ 231

Db 267 LYSKGEERVYECPDY-KTAGPN-SCYFDKKHTSWTIYNTIVKATNEIGSNVSDPLYVD 324
QY 232 LONIYKPLPPVYLTTRSSCEIK-----LKWS-IPGLPIPA--RCFDYIEIREDDTLV 284
Db 325 VYIYVOTDPTPVNTLELKKTKVNRKPYLVLTWSPPLADVRSGWLTLDYELRLKPEA--- 381
QY 285 TATVENYETTLTKTNETRQLCFV-----RSKNVIYCSDD--GIWSEWS-DKOCWEGEDLS 337
Db 382 -----EEWETIFVGOQTHYKMFSLNPGKKYIVQIHCKPDHGSWSELSLEKYLQIPTDFR 436
QY 338 KKTLLRFLWLPFGFILLIVIFV 358
Db 437 IKDMV-VMIIVGLSSLICLV 456

RESULT 7
149280
Interleukin-2 receptor gamma chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R:Cao, X.; Kozak, C.A.; Liu, Y.
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gene
A:Reference number: A47514; MUID:93391374
A:Accession: I49280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <CAO>
A:Cross-references: EMBL:U21795; NID:9727349; PIDN:AAA64279.1; PID:9727350
A:Accession: A47514
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE>
A:Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of function
A:Reference number: JN0592; MUID:93277575
A:Accession: JN0592
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KUM>
A:Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <KOB>
A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
R:Chiu, R.K.; Dougherty, G.G.
submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
A:Reference number: S37582
A:Accession: S37582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:Cross-references: EMBL:X75337
R:DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal location
A:Reference number: I53398; MUID:95104285
A:Accession: I53398
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
C:Genetics:
A:Gene: IL-2Rgamma

A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta
eptors:
A:Description: receptor for interleukin-2
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
F:256-284/Domain: transmembrane #status predicted <TMM>
F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 10.38; Score 212.5; DB 2; Length 369;

Best Local Similarity 26.9%; Pred. No. 1.8e-09;

Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

QY 136 PETKVQDMDCVYVWYLLCSW---KPGIGVLLDTNLYFWYEGLDHAL--OCVDYIK 189
Db 53 PTLPLPEVQCFVFNIEYMNCTWNSSEPOA-----TNLTLYRYKVSNDNTFQEGSHYLF 107
QY 190 ADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIKVPPLPPVYLTFTRE 249
Db 108 SKEITSGCQIQKEDIQLYOTFVWL--QDPQKPORRAVOKLQNLVIPRAPENLTLSNL 165
QY 250 SSECILKWSIPLGPIPARCFDYIEIREDDTLVLTATVENE--TYTLKTTNETRQLCFV 307
Db 166 SESOLELRKW--SRHIKERCLOYLVQYRSNRDRSWTELVNHEPRFSLPSVDELKRYTFR 223
QY 308 VRSYVNIYCSDDGIWSEWSKQCEG-----EDLSKTKTLLEFWLPFGF--ILILVIFVTGL 361
Db 224 VRSYVNIYCSDDGIWSEWSKQCEG-----EDLSKTKTLLEFWLPFGF--ILILVIFVTGL 283
QY 362 LLRKPNTYP 370
Db 284 LERMPPIPP 292

RESULT 8

A55718

Interleukin-2 receptor gamma chain precursor - dog

C:Species: Canis lupus familiaris (dog)

C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999

C:Accession: A55718

R:Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg
Genomics 23, 69-74, 1994

A:Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combi
A:Reference number: A55718; MUID:95130114

A:Accession: A55718

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-373 <HEN>

A:Cross-references: GB:U04361; NID:g517411; PIDN:AAC48403.1; PID:g517412

C:Superfamily: interleukin-2 receptor gamma chain

C:Keywords: cytokine receptor; duplication

Query Match 10.1%; Score 208; DB 2; Length 373;

Best Local Similarity 26.0%; Pred. No. 4.2e-09;

Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;

QY 115 NGSE-----VQSSWAETTWISPOGTPETKVQDMDCVYVWYLLCSW-----KPGI 161
Db 31 NGNEDITPDDFLTATPSET---LSVSSLPLPEVQ---CFVENVEYMNCTWNSSEPRP-- 82
QY 162 GVLLDTNLYFWYEGE--DHALOCVDYIKADGQNGICRFPYLEASDYKDFYICVNGSSE 219
Db 83 -----TNLTLYRYKVSNDNTFQEGSHYLFPSRETAGCWLQKEEHLHYETFWQLDRPE 137
QY 220 NKPTRSSYFTFQLQNIKVPPLPPVYLTFTRESCEIKLKWISPLGPIPARCFDYIEIREDD 279
Db 138 --PRRQSTQKLQNLQNLVIPWAPENLTLSNLSQLELSWS---NRHLDHCLHEVHVQYRSD 192

Query Match	8.8%	Score 180.5;	DB 1;	Length 897;
Best Local Similarity	22.6%	Pred. No. 2e-06;		
Matches	90;	Conservative 58;	Mismatches 146;	Indels 105; Gaps 21;
Qy	32	VNPQDFEIVDPGLGV-----LYLQWQPP-----LSLDHF-----	62	
Db	97	VIPCQSFVTVDVDFEQDPRLCTRLTVLTQHVQPPEDRLQISTDQDFHLTWSVAL	156	
Qy	63	-----KECTVVEYLKRYNIGSETWK--TIIYKNIHLHYKDGFDLNKIGIE-----A	103	
		: : : : : : : : : : : : : : :		
Db	157	GSPOSHWLSPGDLEFEVYVYKRL-QDSWEDAAILLNSNTS-----QATLGPHELMPSSTYVA	210	

[illegible]

Query Match

RESULT 14
A41070
prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 28-Jul-2000
C:Accession: A41070; 155417
R:Ali, S.; Pellegrini, I.; Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin receptor
A:Reference number: A41070; MUID:92041834
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALI>
A:Cross-references: GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390
R:O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin receptor
A:Reference number: 155417; MUID:95014432
A:Accession: 155417
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>
A:Cross-references: EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PID:g641964
A:Experimental source: Nb2-11C cell line
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 8.0%; Score 165; DB 2; Length 412;
Best Local Similarity 28.5%; Pred. No. 1.3e-05;
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;
QY 131 SPQGIPEKVDMDVYNNQYLCSWKPGLVLDNINLFYWEGLDHALQCVDYIKA 190
DB 21 SPQGIPEKVDMDVYNNQYLCSWKPGLVLDNINLFYWEGLDHALQCVDYIKA 190
QY 191 DGQNGICRFPYLEASDYKDFYICVNVN-----GSSENKPIRSSYFTFQLOINIVKPLPPVYLT 245
DB 76 SGPN-SCFESKQYTSIWKYIITVATNQMGSDDPL-----YVDVYIYVEPEPRNLT 129
QY 246 F----TRESSCEIKLWSIP-LGPIPARCF--DYEIEIREDDTTLVATVENET--YTLKTTN-ETRQLCF 300
DB 130 LEVKQLKDKKTYLWVKSPTITDVKTFWEYER-----LKPEAEWEIHTGCH 182
QY 301 TRQL-----CFVRSKVNICYSDGGINSEWSKQWE 332
DB 183 QTFKVFDPYLGQKYLQVTRCK---PDHGYNSRWSQESSVE 220

RESULT 15
I45971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin receptor
A:Reference number: I45971; MUID:93246019
A:Accession: I45971
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:Genetics:
A:Gene: PRLR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 8.0%; Score 165; DB 2; Length 581;

Best Local Similarity 31.3%; Pred. No. 1.9e-05;
Matches 63; Conservative 24; Mismatches 96; Indels 18; Gaps 9;
QY 136 PETKVQDMDCVYNNQYLCSWKPGLVLDNINLFYWEGLDHALQCVDYIKA 195
DB 27 PPEKPKLVKCRSPGKETTCWWEPCADGGLPTNYLTVYHKEGETLIHECPDY-KTGGPN- 84
QY 196 GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLOINIVKPLPPVYLTFTRESSCEIK 255
DB 85 SCYFSKKHTSIWKMYVITVNAINQMGISSDDPLYVHVTVIVEPEPPANLTLELKHPEDRK 144
QY 256 ----LKWSIP-LGPIPARCF--DYEIEIREDDTTLVATVENET--YTLKTTN-ETRQLCF 306
DB 145 PYLWIKWSPTTMDYKSGWFIQYIIRLKPKEAT-----DWETHFTLKQTLKIFNLYP 198
QY 307 VVRSKVNICYSDGGINSEWS 326
DB 199 GOKYLVQINCRPDHGYWSEWS 219

Search completed: September 1, 2001, 19:07:54
Job time: 121 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 1, 2001, 19:15:52 ; Search time 68.62 Seconds
(without alignments)
717.247 Million cell updates/sec

Title: US-09-077-817-2_COPY_1_372
Perfect score: 2056
Sequence: 1 MAFVCLAIGCLYTLISTTF.....ILVIFVTRLRLRPNTYPRM 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_16.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_unclassified.*
- 13: sp_vertebrate.*
- 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194.5	58.1	383	11	O88786
2	310.5	15.1	420	4	Q14633
3	309.5	15.1	396	4	Q14631
4	292	14.2	333	4	Q15469
5	291.5	14.2	415	11	Q920K4
6	264.5	12.9	349	6	O97597
7	241.5	11.7	279	4	Q9UDY5
8	197.5	9.6	363	13	Q9DE01
9	185.5	9.0	611	13	Q9PTI0
10	185.5	9.0	611	13	Q9IBF6
11	178	8.7	896	11	Q64146
12	173.5	8.4	881	13	O57519
13	172	8.4	611	13	Q9PTG9
14	170	8.3	890	11	Q9Z1A0
15	167	8.1	622	6	Q9N0J7
16	165	8.0	296	6	O18880
17	164	8.0	227	6	Q9GLW3
18	159	7.7	581	6	O46561
19	156	7.6	625	6	Q9XS92

20	153.5	7.5	918	13	Q9W609
21	153	7.4	217	6	O46386
22	151	7.3	206	4	Q16354
23	151	7.3	349	4	Q9UHJ5
24	147.5	7.2	538	13	Q9DFU0
25	146.5	7.1	422	4	Q9UHH5
26	145.5	7.1	422	4	O75462
27	143.5	7.0	425	11	Q9JM58
28	138	6.7	390	4	Q9UEH7
29	135	6.6	346	13	Q93404
30	130.5	6.3	198	6	O18985
31	126.5	6.2	329	4	Q9UQ41
32	119.5	5.8	371	4	Q9HC73
33	117.5	5.7	896	4	Q13594
34	117.5	5.7	906	4	Q13593
35	117.5	5.7	958	4	Q13592
36	116.5	5.7	1282	5	Q9VWE0
37	114	5.5	894	6	Q9MYL1
38	114	5.5	925	6	Q9MYK9
39	114	5.5	1163	6	Q9MYL2
40	114	5.5	1194	6	Q9MYL0
41	113.5	5.5	896	4	Q92919
42	113.5	5.5	958	4	Q92920
43	113.5	5.5	1165	4	Q92921
44	111	5.4	628	11	Q9JRG1
45	110	5.4	6875	6	Q28733

ALIGNMENTS

```

RESULT 1
O88786 PRELIMINARY; PRT; 383 AA.
ID O88786;
AC O88786;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IL-13 RECEPTOR ALPHA 2.
GN IL13RA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEJ; TISSUE=THYMUS;
RX MEDLINE=98391042; PubMed=9725226;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,
RA Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,
RA Collins M.;
RT "The murine IL-13 receptor alpha 2: molecular cloning,
RT characterization, and comparison with murine IL-13 receptor alpha 1.";
RL J. Immunol. 161:2317-2324(1998).
DR EMBL; U65747; AAC33240.1; -.
DR MGD; MGI:1277954; IL13ra2.
DR InterPro; IPR002996; -.
DR InterPro; IPR003332; -.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;

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Query Match 58.1%; Score 1194.5; DB 11; Length 383;
Best Local Similarity 58.9%; Pred. No. 1.4e-98;
Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
QY 1 MAFVCLAIGCLYTLISTTFGCTSSSDTEIKVNPDPDFEIVDPGYLYLQWOPPLSD 60
Db 1 MAFV--HIKCLFILLCTTGYS----LEIKVNPDPDFEIVDPGLGYLYLQWPPVIE 54
QY 61 HFKECTVEYELKYNIGSETWTKTITKNIHKGDFLNKGIEAKIHTLPLPWCTNGSEVQ 120
Db 55 KFKGCTLEYELKYNVDSDSWKTIITRNLYKDGFDLNKGIEGKIRTHLSECTNGSEVQ 114

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Qy	121	SSRAETTYWISPOGIPETKVIQODMDCVYYNKNQYLLCSWKPGIGVLLDTNTNLNFYWEGLDH	180
Dd	115	SPWTEASYGISDEGSUETKIQQDMKCIIYNNQYLVCWSKPGKTYSSTNTMTFFWYBEGLDH	174
Qy	181	ALOCVDYIKADGGONICGRFPYLEASDYKOFYICVNGSSENKKPIRSSYFTFQQLNIIVKPLP	240
Dd	175	ALOQCADVLOHDEKNVGCKLSNLDSSDYKOFFICVNGSSKLEPIRSSYTFVQQLNIIVKPLP	234
Qy	241	PVLYTFRRESSCEIKLWSIPLGPPIPARCFDYEIEREDDDTLVTATVSENYTKLTWTNE	300
Dd	235	PEFLHISVENSIDIRMKWSTPGGPPIPRCYTYEIVREDDISWESATDNKMKLKRANE	294
Qy	301	TROLCFVVRSKVNIYSDDGINSWSDKOCWEGEDLSKTLTRFWLPFGFIILIVIFVTG	360
Dd	295	SEDLCFVRCKVNIYCADDGINSEWSEEBECWEGYTGDPDSKII-FIVPVCLFFIFILLLLC	353
Qy	361	LLLRKPNTPTPKM	372
Dd	354	LIVEKEBEPTL	365

RESULT	2
QI14633	
ID	PRELIMINARY; PRT; 420 AA.
AC	QI4633;
DT	01-NOV-1996 (TREMBlrel. 01, Created)
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT	01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE	INTERLEUKIN-5 RECEPTOR PRECURSOR.
DE	HSILSR.
GN	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
[1]	
RN	SEQUENCE FROM N.A.
RC	TISSUE=PERIPHERAL BLOOD;
RX	MEDLINE=92121815; PubMed=1732409;
RA	Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT	"Molecular cloning and expression of the human interleukin 5
RT	receptor.";
RL	J. Exp. Med. 175:341-351(1992).
DR	EMBL; X611176; CAA43483.1; -
DR	InterPro; IPR002996; -
DR	InterPro; IPR003532; -
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW	Signal.
FT	SIGNAL
FT	CHAIN
FT	INTERLEUKIN-5 RECEPTOR.
SQ	SEQUENCE 420 AA; 47670 MW; 8DC560FCB8EFPF524 CRC64;

QY	249	ESSEIKLKWISLPGPAPRCFYETIEIRDDTLTVATVVENETYTKTNNETRQLCFVV	308
		: : : : : :	
Db	250	EGT-RLSIQWEKPVSPAPIHCFHYEVKHTRNGYLQIEKLNFATISIIDLSKYDVQV	308
QY	309	RSKWNIVCSDDGTSWSDSKOCWEGEDLSKTTLLRFWLPGFTILILVFWTGLL	363
		: : : : : :	
Db	309	RAAVSSMCRFAGLWSEWS-QPIYGVNDEHKP---LREW----FVIMATICFILL	356
RESULT	3		
ID	Q14631	PRELIMINARY;	PRT; 396 AA.
AC	Q14631;		
DT	01-NOV-1996	(TEMBRel. 01, Created)	
DT	01-NOV-1996	(TEMBRel. 01, Last sequence update)	
DT	01-MAR-2001	(TEMBRel. 16, Last annotation update)	
DE	INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.		
GN	HSILSR2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_Taxid=9606;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=PERIPHERAL BLOOD;		
RX	MEDLINE=92121815; PubMed=1732409;		
RA	Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.,		
RT	"Molecular cloning and expression of the human interleukin 5		
RT	receptor.";		
RL	J. Exp. Med. 175:341-351(1992).		
EMBL	X61177; CAA43484.1; -.		
InterPro	IPR002996; -.		
DR	InterPro: IPR003532; -.		
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.		
Signal.			
KW	SIGNAL	1	20 POTENTIAL.
FT CHAIN	21	396	INTERLEUKIN-5 RECEPTOR TYPE 2.
SQ	SEQUENCE	396 AA; 44998 MW:	IAB60619842ACDA5 CRC64;

RESULT	4	
Q15469		
ID	Q15469	PRELIMINARY;
AC	Q15469;	PRT; 333 AA.


```
FT NON_TER 349 349
SQ SEQUENCE 349 AA: 39644 MW: D61A4C918B1940A6 CRC64;

Query Match 12.9%; Score 264.5; DB 6; Length 349;
Best Local Similarity 24.4%; Pred. No. 1.2e-15;
Matches 83; Conservative 63; Mismatches 135; Indels 59; Gaps 16;

QY 53 WOPPLSLDFHFKCTVYELKYRNIQSTWKTITIKNLHYKDGFDLNGKTEAKIHTLLPQ 112
Db 18 WNPPEGAS--PNCSLKY---FSHFGNKQDKKAPET-HRSKEVPLNERICLVGS-----Q 67

QY 113 C-TNGSEVOSSWAETTYISPOGIPETKYVODMDCVYNNQYLCSWKPGIGVLLDTNXL 171
Db 68 CSTNESEKPSILVEKCF-SPPEGDPESAVTALQCIWHLNRYMKCTWLPGRNASPDNPYIL 126

QY 172 FYWYEGLDHALQCVYIKADQGNICGRFPYLEASD--YKDFYICVNGSSENKPIRSSFT 229
Db 127 YVHNSLKGILQCNFYR-EGQHIACSFNLTKVKDSSFEQHSVQVMVRDNAGKISPSFNI 185

QY 230 FOLQNIIVKPLPPVYLTFTRESSECEIKLWSIPLGPIPARCFDYEIREDDTTLVTATVE 289
Db 186 VPLTSHVKP-DRSHIKNLFSQGLDYVQWTFNQ-N-FQSCLCYEVEVINSHA----- 235

QY 290 NETYILKTTNTR-----OLCFV-----RSKVNICY-SDDGIWS 323
Db 236 -ETHIDFYVEEAKQNTPEGNLEGTICPMVGLPDTLNTVIRIVKTNKLCYEDDKLWS 294

QY 324 ENSDKOCWEGEDLSKTLRLFWLPGFILLILVFTGLLL 363
Db 295 NWS-----QAMSIGOKANQTFYIT--TLLIIPVIAAAVI 327

RESULT 7
Q9UDY5 PRELIMINARY; PRT; 279 AA.
AC Q9UDY5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81380; AAD00511.2; -
DR HSP; P40189; IBOU.
DR InterPro; IPR002996; -
DR InterPro; IPR003532; -
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 279 AA: 31658 MW: E74141FE9F8E9EBB CRC64;

Query Match 11.7%; Score 241.5; DB 4; Length 279;
Best Local Similarity 27.7%; Pred. No. 1e-13;
Matches 78; Conservative 45; Mismatches 126; Indels 33; Gaps 12;

QY 11 LYTLFLISTFGCTSSSDTEIKVNPQDPFVIDPGVGLYLYLQWQPPSLDHFKECTVEY- 69
Db 10 LWALLCAGGGGGGAAPTETPTPTVNLVSVENLCIVITWNPPEGAS--SNCSLNYF 67

QY 70 ----ELKRVNTGSETWKTITIKNLHYKDGFDLNGKTEAKIHTLLPQ-C-TNGSEVOSSWA 124
Db 68 SHFGDKQDKKAPETRRSI-----EVLNERICLVGS-----QCSSTNESEKPSILV 114

QY 125 ETTYWIS-POGIPETKYVODMDCVYNNQYLCSWKPGIGVLLDTNLYNLYWYEGLDHALQ 183
Db 115 EKC--ISPPEGDSAVTELOQCIWHLNLSYMKCSMLPGRTSPDNTYLYWHRSLKTHQ 172
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QY 184 CVDYIKADQGNICGRFPYLEASD--YKDFYICVNGSSENKPIRSSFTQLQNIIVKPLPP 241
Db 173 C-ENTFREQYGCSCFDLTKVKDSSFEQHSVOIMVKDNAGKIRPFENIVPLTSRVKPDPP 231

QY 242 --VYLTFTRESSECEIKLWSIPLGPIPARCFDYEIREDDT 281
Db 232 HIKNLSFHDN--DLVQWENPQNF-SRCLFYEVEVNSQT 269

RESULT 8
Q9DEQ1 PRELIMINARY; PRT; 363 AA.
AC Q9DEQ1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE CYTOKINE RECEPTOR COMMON GAMMA CHAIN (FRAGMENT).
OC Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RA Wang T., Secombes C.J.;
RL "Cloning and expression of the first non-mammalian cytokine receptor
common gamma chain gene in rainbow trout (Oncorhynchus mykiss).";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276623; CAC09429.1; -
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 363 AA: 41861 MW: DF69B2EE3EEA06D3 CRC64;
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Query Match 9.6%; Score 197.5; DB 13; Length 363;
Best Local Similarity 21.9%; Pred. No. 1.2e-09;
Matches 61; Conservative 56; Mismatches 134; Indels 27; Gaps 9;

QY 97 LNKGEAKIHTLLPWOCTNGSEVOSSWAETTYISPOGIPETKYVODMDCVYNNQYLCS 156
Db 1 IHKYRVELVTLTIPVTHFDMKMGW--LFLLSLQGYEAPSTPNVNCILINDYVNCI 58

QY 157 WKPGIGVLLDTNLYNLYWYEGLDHALQCVYIKADQGNICGRFPYLEASDYKDFYICVNG 216
Db 59 WSE--QSIPEVNTFTFSRFFIKDNMEECTYIQEESYAVGCLSDYKSDRFR----- 108

QY 217 SSENKPIRSSYFTFO---LQNIIVKPLPPVYLTFTRESSECEIKLWSIPLGPIPARCFDY 273
Db 109 TLKTKLVHQNMSYVQDHNLSKLVKLVPPVNLSEVMKDPKELNLYWNSKNTF---CIESE 165

QY 274 IEIREDDTTLVTATVENE-TYLTKTNETRQLCFVVRKVNLYCSDDGIIWSEWSKQWE 332
Db 166 VYRINSKWKTTSTPSEKQYAVAPFLKSSRYEFQVRAVNDMCGESFEWSEWSQPIQWD 225

QY 333 G-----EDLSKTLRLFWLP-FGFIILIVFVTGLL 363
Db 226 SMKGNITDISGSS-MSVWKPVLSLVGTWTLFILACML 262

RESULT 9
Q9PTIO PRELIMINARY; PRT; 611 AA.
AC Q9PTIO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE PROLACTIN RECEPTOR A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
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RN SEQUENCE FROM N.A.
RP MEDLINE=20087225; PubMed=10618394;
RA Huang H., Brown D.D.;
RT "Prolactin is not a juvenile hormone in Xenopus laevis
RT metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL; AF193800; AAF05776.1; -.
DR HSSP; p16471; 1BP3.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 611 AA; 68255 MW; 85629P9P17766FFB6 CRC64;

Query Match          9.0%; Score 185.5; DB 13; Length 611;
Best Local Similarity 28.3%; Pred. No. 2.7e-08;
Matches 71; Conservative 32; Mismatches 109; Indels 39; Gaps 11;

QY 127 TVWISPGIPETKQVDMDCVYNNWQYLLCSWKPGLVLDNTNLFYWYEGDHALQCV 186
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 22 TVSLNAQSLPGKPVID-KCRSEKVTFTSCWKPGLVLDNTNLFYWYEGDHALQCV 80

QY 187 YIKADQNGICRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFQLNIVKPL 239
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 81 YV-TSGLN-SCFFDKAHTSFWIFYHYVYVATNALGNSVDSDESDVTY-----IVQPY 131

QY 240 PPVYLTFRESS-CEIKLKWSIPLGPIPARCFD-----YEIEIRDDTTLVTATVE 289
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 132 PPTNVS LAVESGHDDLLK-----LPPAMVDVQSGWLTLYEYVYKEEKEQWEAHLV 185

QY 290 NETYTLKTTNETRQLCFVVRSKVNIYCS-DDGIWSEWSDKQWEGEDLSKTLRLFWLPF 348
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 186 GNQLKLFGLTPGGNYVQ-----VRCKPDSGHSEWSESYIQIPGGGKTDLTWISI 241

QY 349 GFILLIVIFVT 359
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 242 G-ALSAVIGLT 251

RESULT 10
Q9IBF6 PRELIMINARY; PRT; 611 AA.
AC Q9IBF6;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamamoto T., Nakayama Y., Tajima T., Abe S., Kawahara A.;
RT "Cloning of a cDNA for Xenopus prolactin receptor and its
RT metamorphic expression profile.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030443; BAA0400.1; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 611 AA; 68315 MW; 7E0DF76F21D8CE97 CRC64;

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Query Match          9.0%; Score 185.5; DB 13; Length 611;
Best Local Similarity 28.3%; Pred. No. 2.7e-08;
Matches 71; Conservative 32; Mismatches 109; Indels 39; Gaps 11;

QY 127 TVWISPGIPETKQVDMDCVYNNWQYLLCSWKPGLVLDNTNLFYWYEGDHALQCV 186
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 22 TVSLNAQSLPGKPVID-KCRSEKVTFTSCWKPGLVLDNTNLFYWYEGDHALQCV 80

QY 187 YIKADQNGICRFPYLEASDYKDFYICVNGS-----SENKPIRSSYFTFQLNIVKPL 239
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 81 YV-TSGLN-SCFFDKAHTSFWIFYHYVYVATNALGNSVDSDESDVTY-----IVQPY 131

QY 240 PPVYLTFRESS-CEIKLKWSIPLGPIPARCFD-----YEIEIRDDTTLVTATVE 289
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 132 PPTNVS LAVESGHDDLLK-----LPPAMVDVQSGWLTLYEYVYKEEKEQWEAHLV 185

QY 290 NETYTLKTTNETRQLCFVVRSKVNIYCS-DDGIWSEWSDKQWEGEDLSKTLRLFWLPF 348
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 186 GNQLKLFGLTPGGNYVQ-----VRCKPDSGHSEWSESYIQIPGGGKTDLTWISI 241

QY 349 GFILLIVIFVT 359
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 242 G-ALSAVIGLT 251

RESULT 11
Q64146 PRELIMINARY; PRT; 896 AA.
AC Q64146;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)
DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
GN RIL-3R<BETA>.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370942; PubMed=7643220;
RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
RT microglia and its mRNA expression in vivo.";
RL J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE=BRAIN;
RA Gebicke-Haerter P.J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; S79263; AAB35068.1; -.
DR EMBL; AJ000555; CAA04186.1; -.
DR InterPro; IPR000282; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003531; -.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW SMART; SM00060; FN3; 1.
FT NON_TER 1
FT NON_TER 896
SQ SEQUENCE 896 AA; 99504 MW; 4C5E3B288A4A1052 CRC64;

Query Match          8.7%; Score 178; DB 11; Length 896;
Best Local Similarity 21.4%; Pred. No. 2e-07;
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY 5 CLAIGCL--YT-FLISTTTCGCTSSSDTEIKVN-----PPQDFEIVDPGLVGL 49
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 94 CVPRRCVLPYTFQSVSKEDYISLQPDRLSIHLVPLAQHVQPPPKDISPSG--DHF 151

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QY	50	YLQHQPPL--- <td>106</td>	106
Dd	152	LLKWSVPLGDAQSVLSQKDIQEVAVKQL-QDSWED---ASSLH-----TCNLWVTLEPK	203
QY	107	TLLP-----WQCTNGSEVO---SSWAETTYWISPOGIPETKVQDMDCVVYNMQYILL	154
Dd	204	LFLPNSIVVARVRAQLAPGSSLGRSGSNSPFVHDUSPTE-DKARFONLCQCFDGTQSIN	262
QY	155	CSWKPGIGVLDTNYLNIFYWEGLHALQCVDYIKADQGONIGCRFPYLEASDYKFYICV	214
Dd	263	CSWBWTKVTDSDVSFGLFYSPPKAGEKKCPVVKE-----LQASRYTRVHCSL	311
QY	215	NGSSENPIRSSYFTFOLO-----NIYKLPPP-VYLTFTRESCEIKLKSIDL	262
Dd	312	NVSD---PAHSQTIVSVKRLGOGKTFIESFNHIOMNPPTLNTKNRDS---YSLHWETOK	365
QY	263	GPIPARCDFYEIR-----EDDTTLVTATVENETYITKTNNETROLQFCFVVRKSNVIYC	316
Dd	366	MSYPFIQAFOVQYKKLKLDRWEDSKT----ENLNHAHSMDLPLEPGTSYCARVRVKTIP	421
QY	317	SDDGINSEWDKQCGEDELKSKTLRFLWLPFGFIILIVFYTGLLL	363
Dd	422	EYKGLWSENNECTWT-TDWMMPTL---WT---VLILVFILIUTFL	460

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RESULT 12
057519
ID O57519 PRELIMINARY; PRt; 881 AA.
AC O57519;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE GP130Pl.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RN
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF041845; AAC03531.1; -.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003529; -.
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

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[illegible]

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Db 223 ELISLELPNALKTEWKNPTNFAFNKYNTRYRPVKTQDWEM--VPEEDT-----ASHRDS 276
Qy 293 YTLK-----TTNETRQLCFVVRSKVNIYCSDDGIWSEWSD--KQCV-----EGEDLSKK 339
      :||:      |      |      |      |      |      |      |      |      |      |
Db 277 FTLDLLPNIVYVSIRC-----IHKDGHGFWSDWSELKQKVTPEAPSRGPDWKK 328

RESULT 13
Q9PTH9 Q9PTH9 PRELIMINARY; PRT; 611 AA.
AC AC Q9PTH9;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE PROLACTIN RECEPTOR B.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087225; PubMed=10618394;
RA Huang H., Brown D.D.;
RT "Prolactin is not a juvenile hormone in Xenopus laevis
RL metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:195-199(2000).
DR EMBL; AF193801; AAF05777.1; -.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR001777; -.
DR InterPro; IPR02996; -.
DR InterPro; IPR003528; -.
DR Pfam; PF000041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 611 AA; 69481 MW; CAC658A84A66B313 CRC64;

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Query Match      8.4%; Score 172; DB 13; Length 611;
Best Local Similarity 28.6%; Pred. No. 4.3e-07;
Matches 69; Conservative 30; Mismatches 112; Indels 30; Gaps 11;

QY 131 SPOGIPETKVODMDCVYNNQYLLCSNKPGGICVLDDTNLNFYWEGLDHALOCVDYIKA 190
      ||| ||| : | | ||| | ||| : | | : | | : | | : | | : | | : | | :
Db 29 SPOGKEI-----IKRSYEKVTFCWWRKPSADGGLPNTNLSLYRKENDPKIYECPDY-ET 83
      ||| ||| : | | ||| | ||| : | | : | | : | | : | | : | | : | | :

QY 191 DQONIGRCFPYLEASDKYDFICVNGS-----SENKPIRSSYFTFQLOQNIIVKPLPPVY 243
      ||| ||| : | | ||| | ||| : | | : | | : | | : | | : | | : | | :
Db 84 SGLN-SCYFDKRAHTSFWFYHIVYNNATNALGNSVSEELSDVTY-----IVETYPPTN 135
      ||| ||| : | | ||| | ||| : | | : | | : | | : | | : | | : | | :

QY 244 LTFTPRESS-CBIKLKWSIP-LGPIPA--RCFDYIEIIEIRDDTTLTVAIVENETYLKTTN 299
      ||| ||| : | | ||| | ||| : | | : | | : | | : | | : | | : | | :
Db 136 LSLAVEGDGHLLLVKWHPPDMADVQSGWLTLLKYEVRLEKEEKEQWEAHSVGNQLKLKYG 195
      ||| ||| : | | ||| | ||| : | | : | | : | | : | | : | | : | | :

QY 300 ETRQCLCFVRSKVNLYCS-DGIIWSESDKOCWEGEDLSKTLTLRFWLPFGFILLILVIFV 358
      ||| ||| : | | ||| | ||| : | | : | | : | | : | | : | | : | | :
Db 196 LTPCGNIYVQ---VRCKPDSGHSEWSQESYIQLGGGKTKDMLMLWISVG-TLSAVICL 250
      ||| ||| : | | ||| | ||| : | | : | | : | | : | | : | | : | | :

QY 359 T 359
      |
Db 251 T 251

RESULT 14
Q9Z1A0
AC Q9Z1A0 PRELIMINARY; PRT; 890 AA.
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR BETA CHAIN.
GN IL5.

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RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ272217; CAB75847.1; -.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003528; -.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN1.
DR SMART; SM00060; FN3; 1.
KW Signal; Receptor.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 622 PROLACTIN RECEPTOR.
SQ SEQUENCE 622 AA; 69425 MW; 65F99522C6CD6DB6 CRC64;

Query Match 8.1%; Score 167; DB 6; Length 622;
Best Local Similarity 28.8%; Pred. No. 1.2e-06;
Matches 61; Conservative 26; Mismatches 91; Indels 34; Gaps

QY 131 SPOGIPETKVQDMDCVYVNOVLLCSWKGKIGVLLDTNYNLFVWYEGLDHALQCVDYIKA 190
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 26 SPGKPEI----FKCRSPNKEFTCWMRGADGGLTNTYSLAYHKGEKEFIHECPDYV-T 80
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 191 DGNIGICRFPYLEASDYKDFYICVNGSSSENKPIRSYFTFQLQNIWKPLPPVYLFTRES 250
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 GGNP-SCHFGKQYTSWRVYIITVNATNEMGSTLSDEIIVVDYIIVEPDPPLNV----- 134
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 251 SCEIK-----LKWVIP-LGPIPARCFD--YEIREDDTTLVTATVENETVTLKT 297
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 -VEVKQEDKPKPLWIKWSPPTLIDLKTGWFTLLYEQLKPNAE-----EWETHFAQG 187
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 298 TNETROLCFVRSK--VNIYCS-DDGIWSEWS 326
      : : : : : : : : : : : : : : : : : : : : : :
Db 188 QTDFKVLSLHPGOKYLVQVRCKPDHGYWSWS 219
      : : : : : : : : : : : : : : : : : : : : : :

Search completed: September 1, 2001, 19:15:53
Job time: 525 sec

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